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| GR NAME | GR DESCRIPTION |
|---|---|

GR1 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 1(GR1) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR1 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR1 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR1 precursor DNA encodes GR1 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR1 is located from position 79828330 to position 79828455 relative to chromosome 14 on the `-` strand.

GR1 precursor RNA folds spatially, forming GR1 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR1 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR1 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR1 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2807 precursor RNA and GAM4147 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2807 RNA and GAM4147 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2807 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2807 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2807 target RNA into GAM2807 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4147 RNA, herein schematically represented by GAM1 RNA through GAM3

RNA, binds complementarily to a target binding site located in an untranslated region of GAM4147 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4147 target RNA into GAM4147 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR1 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR1 polynucleotide: GAM2807 target protein and GAM4147 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM2807 and GAM4147

GR2 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 2(GR2) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR2 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR2 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR2 precursor DNA encodes GR2 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR2 is located from position 25868146 to position 25868249 relative to chromosome 21 on the `+` strand.

GR2 precursor RNA folds spatially, forming GR2 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR2 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR2 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2543 precursor RNA and GAM4738 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2543 RNA and GAM4738 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2543 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2543 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2543 target RNA into GAM2543 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4738 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4738 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4738 target RNA into GAM4738 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR2 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR2 polynucleotide: GAM2543 target protein and GAM4738 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM2543 and GAM4738

GR3 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 3(GR3) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR3 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR3 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR3 precursor DNA encodes GR3 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR3 is located from position 3260143 to position 3260219 relative to chromosome 7 on the `-` strand.

GR3 precursor RNA folds spatially, forming GR3 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3 folded precursor RNA comprises a plurality of what is known in the art as `hairpin`

structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR3 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR3 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7530 precursor RNA and GAM7933 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7530 RNA and GAM7933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7530 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7530 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7530 target RNA into GAM7530 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7933 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7933 target RNA into GAM7933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR3 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR3 polynucleotide: GAM7530 target protein and GAM7933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM7530 and GAM7933

GR4 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 4(GR4) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR4 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR4 precursor DNA encodes GR4 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR4 is located from position 131248823 to position 131249168 relative to chromosome X on the `-` strand.

GR4 precursor RNA folds spatially, forming GR4 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR4 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2608 precursor RNA and GAM3298 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2608 RNA and GAM3298 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2608 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2608 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2608 target RNA into GAM2608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3298 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3298 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3298 target RNA into GAM3298 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4 polynucleotide: GAM2608 target protein and GAM3298 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM2608 and GAM3298

GR5 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 5(GR5) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR5 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR5 precursor DNA encodes GR5 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR5 is located from position 39394031 to position 39394119 relative to chromosome 1 on the `+` strand.

GR5 precursor RNA folds spatially, forming GR5 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR5 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336704 precursor RNA and GAM336705 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336704 RNA and GAM336705 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336704 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336704 target RNA into GAM336704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336705 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336705 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336705 target RNA into GAM336705 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5 polynucleotide: GAM336704 target protein and GAM336705 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336704 and GAM336705

GR6 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 6(GR6) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR6 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR6 precursor DNA encodes GR6 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR6 is located from position 158626687 to position 158626807 relative to chromosome 1 on the `+` strand.

GR6 precursor RNA folds spatially, forming GR6 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR6 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM

precursor RNAs, GAM4561 precursor RNA and GAM8285 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4561 RNA and GAM8285 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4561 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4561 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4561 target RNA into GAM4561 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8285 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8285 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8285 target RNA into GAM8285 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6 polynucleotide: GAM4561 target protein and GAM8285 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4561 and GAM8285

GR7 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 7(GR7) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR7 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR7 precursor DNA encodes GR7 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long. Nucleotide sequence of GR7 is located from position 12778141 to position 12778255 relative to chromosome 10 on the `+` strand.

GR7 precursor RNA folds spatially, forming GR7 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR7 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336388 precursor RNA and GAM336389 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336388 RNA and GAM336389 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336388 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336388 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336388 target RNA into GAM336388 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336389 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336389 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336389 target RNA into GAM336389 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7 polynucleotide: GAM336388 target protein and GAM336389 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336388 and GAM336389

GR8 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 8(GR8) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR8 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR8 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR8 precursor DNA encodes GR8 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR8 is located from position 70411479 to position 70411571 relative to chromosome 10 on the `+` strand.

GR8 precursor RNA folds spatially, forming GR8 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR8 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR8 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR8 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337083 precursor RNA and GAM337084 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337083 RNA and GAM337084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337083 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337083 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337083 target RNA into GAM337083 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337084 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337084 target RNA into GAM337084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR8 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR8 polynucleotide: GAM337083 target protein and GAM337084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337083 and GAM337084

GR9 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 9(GR9) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR9 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR9 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR9 precursor DNA encodes GR9 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR9 is located from position 101743922 to position 101744005 relative to chromosome 10 on the `+` strand.

GR9 precursor RNA folds spatially, forming GR9 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR9 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR9 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR9 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM892 precursor RNA and GAM5886 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM892 RNA and GAM5886 RNA, herein schematically represented by GAM1

RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM892 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM892 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM892 target RNA into GAM892 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5886 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5886 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5886 target RNA into GAM5886 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR9 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR9 polynucleotide: GAM892 target protein and GAM5886 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM892 and GAM5886

GR10 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 10(GR10) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR10 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR10 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR10 precursor DNA encodes GR10 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR10 is located from position 121833616 to position 121833747 relative to chromosome 10 on the `+` strand.

GR10 precursor RNA folds spatially, forming GR10 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR10 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR10 precursor RNA comprises a plurality of segments, the first half

of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR10 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM367 precursor RNA and GAM6807 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM367 RNA and GAM6807 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM367 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM367 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM367 target RNA into GAM367 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6807 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6807 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6807 target RNA into GAM6807 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR10 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR10 polynucleotide: GAM367 target protein and GAM6807 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM367 and GAM6807

GR11 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 11(GR11) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR11 precursor DNA, herein designated GR PRECURSOR DNA, is a novel

bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR11 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR11 precursor DNA encodes GR11 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR11 is located from position 15010865 to position 15010960 relative to chromosome 10 on the `-` strand.

GR11 precursor RNA folds spatially, forming GR11 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR11 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR11 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR11 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM336407 precursor RNA, GAM336408 precursor RNA and GAM336409 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336407 RNA, GAM336408 RNA and GAM336409 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336407 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336407 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336407 target RNA into GAM336407 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336408 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336408 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336408 target RNA into GAM336408 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336409 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM336409 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336409 target RNA into GAM336409 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR11 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR11 polynucleotide: GAM336407 target protein, GAM336408 target protein and GAM336409 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336407, GAM336408 and GAM336409

GR12 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 12(GR12) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR12 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR12 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR12 precursor DNA encodes GR12 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR12 is located from position 22440215 to position 22440312 relative to chromosome 10 on the `-` strand.

GR12 precursor RNA folds spatially, forming GR12 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR12 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR12 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR12 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336507 precursor RNA and GAM336508 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336507 RNA and GAM336508 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336507 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336507 target RNA into GAM336507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336508 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336508 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336508 target RNA into GAM336508 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR12 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR12 polynucleotide: GAM336507 target protein and GAM336508 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336507 and GAM336508

GR13 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 13(GR13) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR13 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR13 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR13 precursor DNA encodes GR13 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR13 is located from position 93938738 to position 93938849 relative to chromosome 10 on the `-` strand.

GR13 precursor RNA folds spatially, forming GR13 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR13 folded precursor RNA comprises a plurality of what is known in the art as `hairpin`

structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR13 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR13 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1914 precursor RNA and GAM3271 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1914 RNA and GAM3271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1914 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1914 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1914 target RNA into GAM1914 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3271 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3271 target RNA into GAM3271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR13 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR13 polynucleotide: GAM1914 target protein and GAM3271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1914 and GAM3271

GR14 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 14(GR14) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR14 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR14 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR14 precursor DNA encodes GR14 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR14 is located from position 94365822 to position 94365930 relative to chromosome 10 on the `-` strand.

GR14 precursor RNA folds spatially, forming GR14 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR14 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR14 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR14 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337270 precursor RNA and GAM337271 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337270 RNA and GAM337271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337270 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337270 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337270 target RNA into GAM337270 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337271 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337271 target RNA into GAM337271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR14 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR14 polynucleotide: GAM337270 target protein and GAM337271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337270 and GAM337271

GR15 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 15(GR15) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR15 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR15 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR15 precursor DNA encodes GR15 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR15 is located from position 102859212 to position 102859318 relative to chromosome 10 on the `-` strand.

GR15 precursor RNA folds spatially, forming GR15 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR15 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR15 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR15 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1523 precursor RNA and GAM7654 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1523 RNA and GAM7654 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1523 target RNA, herein schematically represented by GAM1 TARGET RNA

through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1523 target RNA into GAM1523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7654 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7654 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7654 target RNA into GAM7654 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR15 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR15 polynucleotide: GAM1523 target protein and GAM7654 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1523 and GAM7654

GR16 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 16(GR16) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR16 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR16 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR16 precursor DNA encodes GR16 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR16 is located from position 105033873 to position 105033967 relative to chromosome 10 on the `-` strand.

GR16 precursor RNA folds spatially, forming GR16 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR16 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR16 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR16 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate

GAM precursor RNAs, GAM337377 precursor RNA and GAM337378 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337377 RNA and GAM337378 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337377 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337377 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337377 target RNA into GAM337377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337378 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337378 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337378 target RNA into GAM337378 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR16 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR16 polynucleotide: GAM337377 target protein and GAM337378 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337377 and GAM337378

GR17 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 17(GR17) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR17 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR17 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR17 precursor DNA encodes GR17 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long. Nucleotide sequence of GR17 is located from position 105533378 to position 105533458 relative to chromosome 10 on the `-` strand.

GR17 precursor RNA folds spatially, forming GR17 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR17 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR17 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR17 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1087 precursor RNA and GAM8693 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1087 RNA and GAM8693 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1087 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1087 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1087 target RNA into GAM1087 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8693 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8693 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8693 target RNA into GAM8693 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR17 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR17 polynucleotide: GAM1087 target protein and GAM8693 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1087 and GAM8693

GR18 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 18(GR18) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR18 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR18 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR18 precursor DNA encodes GR18 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR18 is located from position 48222373 to position 48222452 relative to chromosome 11 on the `+` strand.

GR18 precursor RNA folds spatially, forming GR18 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR18 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR18 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR18 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM44 precursor RNA and GAM83 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM44 RNA and GAM83 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM44 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM44 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM44 target RNA into GAM44 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM83 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83 target RNA into GAM83 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR18 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR18 polynucleotide: GAM44 target protein and GAM83 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM44 and GAM83

GR19 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 19(GR19) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR19 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR19 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR19 precursor DNA encodes GR19 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR19 is located from position 92812990 to position 92813083 relative to chromosome 11 on the `+` strand.

GR19 precursor RNA folds spatially, forming GR19 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR19 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR19 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR19 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1860 precursor RNA and GAM7601 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1860 RNA and GAM7601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig.

8.

GAM1860 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1860 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1860 target RNA into GAM1860 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7601 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7601 target RNA into GAM7601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR19 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR19 polynucleotide: GAM1860 target protein and GAM7601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1860 and GAM7601

GR20 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 20(GR20) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR20 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR20 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR20 precursor DNA encodes GR20 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR20 is located from position 113128395 to position 113128479 relative to chromosome 11 on the `+` strand.

GR20 precursor RNA folds spatially, forming GR20 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR20 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR20 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or

accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR20 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337441 precursor RNA, GAM337442 precursor RNA and GAM337443 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337441 RNA, GAM337442 RNA and GAM337443 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337441 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337441 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337441 target RNA into GAM337441 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337442 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337442 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337442 target RNA into GAM337442 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337443 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337443 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337443 target RNA into GAM337443 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR20 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR20 polynucleotide: GAM337441 target protein, GAM337442 target protein and GAM337443 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337441, GAM337442 and GAM337443

GR21 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 21(GR21) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR21 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR21 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR21 precursor DNA encodes GR21 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR21 is located from position 45420363 to position 45420459 relative to chromosome 11 on the `-` strand.

GR21 precursor RNA folds spatially, forming GR21 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR21 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR21 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR21 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM588 precursor RNA and GAM1440 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM588 RNA and GAM1440 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM588 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM588 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM588 target RNA into GAM588 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM1440 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated

region of GAM1440 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1440 target RNA into GAM1440 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR21 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR21 polynucleotide: GAM588 target protein and GAM1440 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM588 and GAM1440

GR22 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 22(GR22) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR22 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR22 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR22 precursor DNA encodes GR22 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR22 is located from position 69517026 to position 69517124 relative to chromosome 11 on the `-` strand.

GR22 precursor RNA folds spatially, forming GR22 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR22 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR22 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR22 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2887 precursor RNA and GAM6083 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides

in length, GAM2887 RNA and GAM6083 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2887 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2887 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2887 target RNA into GAM2887 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6083 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6083 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6083 target RNA into GAM6083 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR22 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR22 polynucleotide: GAM2887 target protein and GAM6083 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM2887 and GAM6083

GR23 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 23(GR23) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR23 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR23 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR23 precursor DNA encodes GR23 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR23 is located from position 78654885 to position 78654989 relative to chromosome 11 on the `-` strand.

GR23 precursor RNA folds spatially, forming GR23 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR23 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide

sequence of GR23 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR23 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3630 precursor RNA and GAM7264 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3630 RNA and GAM7264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3630 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3630 target RNA into GAM3630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7264 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7264 target RNA into GAM7264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR23 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR23 polynucleotide: GAM3630 target protein and GAM7264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM3630 and GAM7264

GR24 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 24(GR24) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR24 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR24 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR24 precursor DNA encodes GR24 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR24 is located from position 96304357 to position 96304458 relative to chromosome 11 on the `-` strand.

GR24 precursor RNA folds spatially, forming GR24 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR24 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR24 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR24 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5292 precursor RNA and GAM7777 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5292 RNA and GAM7777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5292 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5292 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5292 target RNA into GAM5292 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7777 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7777 target RNA into GAM7777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities,

of GR24 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR24 polynucleotide: GAM5292 target protein and GAM7777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM5292 and GAM7777

GR25 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 25(GR25) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR25 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR25 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR25 precursor DNA encodes GR25 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR25 is located from position 116689623 to position 116689733 relative to chromosome 11 on the `-` strand.

GR25 precursor RNA folds spatially, forming GR25 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR25 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR25 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR25 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337458 precursor RNA and GAM337459 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337458 RNA and GAM337459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337458 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337458 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to

a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337458 target RNA into GAM337458 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337459 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337459 target RNA into GAM337459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR25 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR25 polynucleotide: GAM337458 target protein and GAM337459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337458 and GAM337459

GR26 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 26(GR26) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR26 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR26 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR26 precursor DNA encodes GR26 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR26 is located from position 46553863 to position 46553950 relative to chromosome 12 on the `+` strand.

GR26 precursor RNA folds spatially, forming GR26 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR26 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR26 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR26 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM270 precursor RNA and GAM965 precursor RNA,herein

schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM270 RNA and GAM965 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM270 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270 target RNA into GAM270 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM965 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM965 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM965 target RNA into GAM965 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR26 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR26 polynucleotide: GAM270 target protein and GAM965 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM270 and GAM965

GR27 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 27(GR27) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR27 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR27 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR27 precursor DNA encodes GR27 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR27 is located from position 53823632

to position 53823727 relative to chromosome 12 on the `-` strand.

GR27 precursor RNA folds spatially, forming GR27 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR27 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR27 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR27 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336892 precursor RNA and GAM336893 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336892 RNA and GAM336893 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336892 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336892 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336892 target RNA into GAM336892 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336893 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336893 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336893 target RNA into GAM336893 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR27 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR27 polynucleotide: GAM336892 target protein and GAM336893 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336892 and GAM336893

GR28 Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory polynucleotide, referred to here as Genomic Record 28(GR28) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR28 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR28 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR28 precursor DNA encodes GR28 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR28 is located from position 56320934 to position 56321065 relative to chromosome 12 on the `-` strand.

GR28 precursor RNA folds spatially, forming GR28 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR28 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR28 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR28 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5868 precursor RNA and GAM6799 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5868 RNA and GAM6799 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5868 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5868 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5868 target RNA into GAM5868 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6799 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6799 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6799 target RNA into GAM6799 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR28 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR28 polynucleotide: GAM5868 target protein and GAM6799 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM5868 and GAM6799

GR29 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 29(GR29) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR29 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR29 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR29 precursor DNA encodes GR29 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR29 is located from position 56423119 to position 56423221 relative to chromosome 12 on the `-` strand.

GR29 precursor RNA folds spatially, forming GR29 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR29 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR29 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR29 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336906 precursor RNA and GAM336907 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336906 RNA and GAM336907 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of

Fig. 8.

GAM336906 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336906 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336906 target RNA into GAM336906 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336907 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336907 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336907 target RNA into GAM336907 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR29 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR29 polynucleotide: GAM336906 target protein and GAM336907 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336906 and GAM336907

GR30 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 30(GR30) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR30 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR30 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR30 precursor DNA encodes GR30 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR30 is located from position 56453734 to position 56453831 relative to chromosome 12 on the `-` strand.

GR30 precursor RNA folds spatially, forming GR30 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR30 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR30 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or

accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR30 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1293 precursor RNA and GAM6306 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1293 RNA and GAM6306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1293 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1293 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1293 target RNA into GAM1293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6306 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6306 target RNA into GAM6306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR30 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR30 polynucleotide: GAM1293 target protein and GAM6306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1293 and GAM6306

GR31 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 31(GR31) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR31 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The

method by which GR31 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR31 precursor DNA encodes GR31 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR31 is located from position 56716065 to position 56716147 relative to chromosome 12 on the `-` strand.

GR31 precursor RNA folds spatially, forming GR31 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR31 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR31 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR31 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336913 precursor RNA and GAM336914 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336913 RNA and GAM336914 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336913 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336913 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336913 target RNA into GAM336913 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336914 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336914 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336914 target RNA into GAM336914 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR31 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like`

cluster of GR31 polynucleotide: GAM336913 target protein and GAM336914 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336913 and GAM336914

GR32 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 32(GR32) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR32 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR32 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR32 precursor DNA encodes GR32 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR32 is located from position 70649160 to position 70649248 relative to chromosome 12 on the `-` strand.

GR32 precursor RNA folds spatially, forming GR32 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR32 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR32 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR32 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337088 precursor RNA and GAM337089 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337088 RNA and GAM337089 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337088 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337088 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337088 target RNA into GAM337088

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337089 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337089 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337089 target RNA into GAM337089 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR32 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR32 polynucleotide: GAM337088 target protein and GAM337089 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337088 and GAM337089

GR33 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 33(GR33) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR33 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR33 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR33 precursor DNA encodes GR33 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR33 is located from position 96681277 to position 96681380 relative to chromosome 12 on the `-` strand.

GR33 precursor RNA folds spatially, forming GR33 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR33 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR33 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR33 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337288 precursor RNA and GAM337289 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA

segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337288 RNA and GAM337289 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337288 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337288 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337288 target RNA into GAM337288 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337289 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337289 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337289 target RNA into GAM337289 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR33 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR33 polynucleotide: GAM337288 target protein and GAM337289 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337288 and GAM337289

GR34 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 34(GR34) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR34 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR34 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR34 precursor DNA encodes GR34 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR34 is located from position 26088279 to position 26088406 relative to chromosome 13 on the `+` strand.

GR34 precursor RNA folds spatially, forming GR34 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR34 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR34 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR34 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1144 precursor RNA and GAM7369 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1144 RNA and GAM7369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1144 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1144 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1144 target RNA into GAM1144 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7369 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7369 target RNA into GAM7369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR34 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR34 polynucleotide: GAM1144 target protein and GAM7369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1144 and GAM7369

GR35 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 35(GR35) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like

oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR35 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR35 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR35 precursor DNA encodes GR35 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR35 is located from position 97963174 to position 97963274 relative to chromosome 13 on the `-` strand.

GR35 precursor RNA folds spatially, forming GR35 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR35 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR35 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR35 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337296 precursor RNA and GAM337297 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337296 RNA and GAM337297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337296 target RNA into GAM337296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337297 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337297 target RNA into GAM337297

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR35 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR35 polynucleotide: GAM337296 target protein and GAM337297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337296 and GAM337297

GR36 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 36(GR36) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR36 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR36 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR36 precursor DNA encodes GR36 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR36 is located from position 110102077 to position 110102191 relative to chromosome 13 on the `-` strand.

GR36 precursor RNA folds spatially, forming GR36 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR36 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR36 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR36 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4205 precursor RNA and GAM6811 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4205 RNA and GAM6811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4205 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4205 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4205 target RNA into GAM4205 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6811 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6811 target RNA into GAM6811 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR36 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR36 polynucleotide: GAM4205 target protein and GAM6811 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4205 and GAM6811

GR37 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 37(GR37) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR37 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR37 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR37 precursor DNA encodes GR37 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR37 is located from position 62330677 to position 62330789 relative to chromosome 14 on the `+` strand.

GR37 precursor RNA folds spatially, forming GR37 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR37 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR37 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR37 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336965 precursor RNA and GAM336966 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336965 RNA and GAM336966 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336965 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336965 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336965 target RNA into GAM336965 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336966 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336966 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336966 target RNA into GAM336966 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR37 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR37 polynucleotide: GAM336965 target protein and GAM336966 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336965 and GAM336966

GR38 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 38(GR38) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR38 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR38 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR38 precursor DNA encodes GR38 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR38 is located from position 86637061 to position 86637148 relative to chromosome 14 on the `+` strand.

GR38 precursor RNA folds spatially, forming GR38 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR38 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR38 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR38 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM933 precursor RNA and GAM4008 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM933 RNA and GAM4008 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM933 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM933 target RNA into GAM933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4008 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4008 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4008 target RNA into GAM4008 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR38 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR38 polynucleotide: GAM933 target protein and GAM4008 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET

PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM933 and GAM4008

GR39 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 39(GR39) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR39 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR39 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR39 precursor DNA encodes GR39 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR39 is located from position 92455725 to position 92455812 relative to chromosome 14 on the `+` strand.

GR39 precursor RNA folds spatially, forming GR39 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR39 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR39 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR39 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337255 precursor RNA and GAM337256 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337255 RNA and GAM337256 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337255 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337255 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337255 target RNA into GAM337255 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337256 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337256 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337256 target RNA into GAM337256 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR39 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR39 polynucleotide: GAM337255 target protein and GAM337256 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337255 and GAM337256

GR40 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 40(GR40) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR40 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR40 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR40 precursor DNA encodes GR40 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR40 is located from position 93614973 to position 93615067 relative to chromosome 14 on the `+` strand.

GR40 precursor RNA folds spatially, forming GR40 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR40 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR40 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR40 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1332 precursor RNA and GAM8636 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1332 RNA and GAM8636 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1332 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1332 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1332 target RNA into GAM1332 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8636 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8636 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8636 target RNA into GAM8636 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR40 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR40 polynucleotide: GAM1332 target protein and GAM8636 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1332 and GAM8636

GR41 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 41(GR41) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR41 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR41 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR41 precursor DNA encodes GR41 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR41 is located from position 62113790 to position 62113885 relative to chromosome 14 on the `-` strand.

GR41 precursor RNA folds spatially, forming GR41 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR41 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR41 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR41 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM408 precursor RNA and GAM1431 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM408 RNA and GAM1431 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM408 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM408 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM408 target RNA into GAM408 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM1431 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1431 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1431 target RNA into GAM1431 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR41 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR41 polynucleotide: GAM408 target protein and GAM1431 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM408 and GAM1431

GR42 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 42(GR42) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known

in the art.

GR42 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR42 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR42 precursor DNA encodes GR42 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR42 is located from position 89325453 to position 89325536 relative to chromosome 14 on the `-` strand.

GR42 precursor RNA folds spatially, forming GR42 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR42 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR42 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR42 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337233 precursor RNA, GAM337234 precursor RNA and GAM337235 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337233 RNA, GAM337234 RNA and GAM337235 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337233 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337233 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337233 target RNA into GAM337233 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337234 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337234 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337234 target RNA into GAM337234 target protein, herein schematically represented by GAM1 TARGET PROTEIN through

GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337235 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337235 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337235 target RNA into GAM337235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR42 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR42 polynucleotide: GAM337233 target protein, GAM337234 target protein and GAM337235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337233, GAM337234 and GAM337235

GR43 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 43(GR43) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR43 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR43 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR43 precursor DNA encodes GR43 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR43 is located from position 40608762 to position 40608869 relative to chromosome 15 on the `+` strand.

GR43 precursor RNA folds spatially, forming GR43 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR43 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR43 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR43 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM507 precursor RNA and GAM1295 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA

segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM507 RNA and GAM1295 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM507 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM507 target RNA into GAM507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM1295 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1295 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1295 target RNA into GAM1295 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR43 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR43 polynucleotide: GAM507 target protein and GAM1295 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM507 and GAM1295

GR44 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 44(GR44) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR44 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR44 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR44 precursor DNA encodes GR44 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR44 is located from position 24278760 to position 24278861 relative to chromosome 15 on the `-` strand.

GR44 precursor RNA folds spatially, forming GR44 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR44 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR44 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR44 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336532 precursor RNA and GAM336533 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336532 RNA and GAM336533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336532 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336532 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336532 target RNA into GAM336532 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336533 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336533 target RNA into GAM336533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR44 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR44 polynucleotide: GAM336532 target protein and GAM336533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336532 and GAM336533

GR45 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 45(GR45) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like

oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR45 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR45 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR45 precursor DNA encodes GR45 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR45 is located from position 53161338 to position 53161431 relative to chromosome 15 on the `-` strand.

GR45 precursor RNA folds spatially, forming GR45 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR45 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR45 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR45 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4538 precursor RNA and GAM7302 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4538 RNA and GAM7302 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4538 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4538 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4538 target RNA into GAM4538 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7302 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7302 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7302 target RNA into GAM7302 target

protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR45 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR45 polynucleotide: GAM4538 target protein and GAM7302 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4538 and GAM7302

GR46 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 46(GR46) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR46 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR46 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR46 precursor DNA encodes GR46 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR46 is located from position 53974892 to position 53975006 relative to chromosome 15 on the `-` strand.

GR46 precursor RNA folds spatially, forming GR46 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR46 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR46 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR46 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM807 precursor RNA, GAM2808 precursor RNA and GAM3132 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM807 RNA, GAM2808 RNA and GAM3132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM807 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM807 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM807 target RNA into GAM807 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2808 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2808 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2808 target RNA into GAM2808 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3132 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3132 target RNA into GAM3132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR46 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR46 polynucleotide: GAM807 target protein, GAM2808 target protein and GAM3132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM807, GAM2808 and GAM3132

GR47 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 47(GR47) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR47 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR47 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR47 precursor DNA encodes GR47 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR47 is located from position 90601712 to position 90601949 relative to chromosome 15 on the `-` strand.

GR47 precursor RNA folds spatially, forming GR47 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR47 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR47 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR47 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4800 precursor RNA and GAM5958 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4800 RNA and GAM5958 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4800 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4800 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4800 target RNA into GAM4800 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5958 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5958 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5958 target RNA into GAM5958 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR47 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR47 polynucleotide: GAM4800 target protein and GAM5958 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4800 and GAM5958

GR48 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 48(GR48)

polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR48 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR48 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR48 precursor DNA encodes GR48 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR48 is located from position 94819576 to position 94819679 relative to chromosome 15 on the `-` strand.

GR48 precursor RNA folds spatially, forming GR48 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR48 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR48 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR48 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337274 precursor RNA and GAM337275 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337274 RNA and GAM337275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337274 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337274 target RNA into GAM337274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337275 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig. 8, thereby inhibiting translation of GAM337275 target RNA into GAM337275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR48 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR48 polynucleotide: GAM337274 target protein and GAM337275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337274 and GAM337275

GR49 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 49(GR49) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR49 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR49 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR49 precursor DNA encodes GR49 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR49 is located from position 20421189 to position 20421286 relative to chromosome 16 on the `+` strand.

GR49 precursor RNA folds spatially, forming GR49 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR49 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR49 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR49 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336477 precursor RNA and GAM336478 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336477 RNA and GAM336478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336477 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336477 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336477 target RNA into GAM336477 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336478 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336478 target RNA into GAM336478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR49 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR49 polynucleotide: GAM336477 target protein and GAM336478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336477 and GAM336478

GR50 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 50(GR50) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR50 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR50 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR50 precursor DNA encodes GR50 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR50 is located from position 24755757 to position 24755840 relative to chromosome 16 on the `+` strand.

GR50 precursor RNA folds spatially, forming GR50 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR50 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR50 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known

in the art.

GR50 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336537 precursor RNA and GAM336538 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336537 RNA and GAM336538 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336537 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336537 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336537 target RNA into GAM336537 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336538 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336538 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336538 target RNA into GAM336538 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR50 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR50 polynucleotide: GAM336537 target protein and GAM336538 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336537 and GAM336538

GR51 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 51(GR51) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR51 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR51 precursor DNA was detected is described hereinabove with

additional reference to Figs. 8-18.

GR51 precursor DNA encodes GR51 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR51 is located from position 78245362 to position 78245462 relative to chromosome 16 on the `+` strand.

GR51 precursor RNA folds spatially, forming GR51 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR51 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR51 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR51 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337185 precursor RNA and GAM337186 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337185 RNA and GAM337186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337185 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337185 target RNA into GAM337185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337186 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337186 target RNA into GAM337186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR51 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR51 polynucleotide: GAM337185 target protein and GAM337186 target

protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337185 and GAM337186

GR52 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 52(GR52) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR52 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR52 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR52 precursor DNA encodes GR52 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR52 is located from position 15101510 to position 15101597 relative to chromosome 16 on the `-` strand.

GR52 precursor RNA folds spatially, forming GR52 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR52 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR52 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR52 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2817 precursor RNA and GAM4844 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2817 RNA and GAM4844 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2817 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2817 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2817 target RNA into GAM2817 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3

TARGET PROTEIN, both of Fig. 8.

GAM4844 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4844 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4844 target RNA into GAM4844 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR52 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR52 polynucleotide: GAM2817 target protein and GAM4844 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM2817 and GAM4844

GR53 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 53(GR53) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR53 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR53 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR53 precursor DNA encodes GR53 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR53 is located from position 20480066 to position 20480163 relative to chromosome 16 on the `-` strand.

GR53 precursor RNA folds spatially, forming GR53 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR53 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR53 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR53 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336479 precursor RNA and GAM336480 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336479 RNA and GAM336480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336479 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336479 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336479 target RNA into GAM336479 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336480 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336480 target RNA into GAM336480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR53 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR53 polynucleotide: GAM336479 target protein and GAM336480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336479 and GAM336480

GR54 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 54(GR54) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR54 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR54 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR54 precursor DNA encodes GR54 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR54 is located from position 30319063 to position 30319173 relative to chromosome 17 on the `+` strand.

GR54 precursor RNA folds spatially, forming GR54 folded precursor RNA,

herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR54 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR54 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR54 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM785 precursor RNA and GAM8631 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM785 RNA and GAM8631 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM785 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM785 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM785 target RNA into GAM785 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8631 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8631 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8631 target RNA into GAM8631 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR54 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR54 polynucleotide: GAM785 target protein and GAM8631 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM785 and GAM8631

GR55 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 55(GR55) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR55 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR55 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR55 precursor DNA encodes GR55 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR55 is located from position 40086542 to position 40086976 relative to chromosome 17 on the `+` strand.

GR55 precursor RNA folds spatially, forming GR55 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR55 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR55 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR55 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4423 precursor RNA and GAM336720 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4423 RNA and GAM336720 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4423 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4423 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4423 target RNA into GAM4423 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336720 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336720 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336720 target RNA into GAM336720 target protein, herein schematically represented by GAM1 TARGET PROTEIN through

GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR55 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR55 polynucleotide: GAM4423 target protein and GAM336720 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4423 and GAM336720

GR56 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 56(GR56) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR56 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR56 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR56 precursor DNA encodes GR56 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR56 is located from position 43395837 to position 43395938 relative to chromosome 17 on the `+` strand.

GR56 precursor RNA folds spatially, forming GR56 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR56 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR56 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR56 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM674 precursor RNA and GAM3126 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM674 RNA and GAM3126 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM674 RNA, herein schematically represented by GAM1 RNA through GAM3

RNA, binds complementarily to a target binding site located in an untranslated region of GAM674 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM674 target RNA into GAM674 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3126 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3126 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3126 target RNA into GAM3126 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR56 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR56 polynucleotide: GAM674 target protein and GAM3126 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM674 and GAM3126

GR57 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 57(GR57) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR57 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR57 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR57 precursor DNA encodes GR57 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR57 is located from position 78873540 to position 78873673 relative to chromosome 17 on the `+` strand.

GR57 precursor RNA folds spatially, forming GR57 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR57 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR57 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR57 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2868 precursor RNA, GAM6466 precursor RNA and GAM6564 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2868 RNA, GAM6466 RNA and GAM6564 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2868 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2868 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2868 target RNA into GAM2868 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6466 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6466 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6466 target RNA into GAM6466 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6564 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6564 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6564 target RNA into GAM6564 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR57 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR57 polynucleotide: GAM2868 target protein, GAM6466 target protein and GAM6564 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM2868, GAM6466 and GAM6564

GR58 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 58(GR58) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like

oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR58 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR58 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR58 precursor DNA encodes GR58 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR58 is located from position 1319182 to position 1319275 relative to chromosome 17 on the `-` strand.

GR58 precursor RNA folds spatially, forming GR58 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR58 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR58 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR58 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM842 precursor RNA and GAM2920 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM842 RNA and GAM2920 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM842 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM842 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM842 target RNA into GAM842 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2920 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2920 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2920 target RNA into GAM2920 target

protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR58 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR58 polynucleotide: GAM842 target protein and GAM2920 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM842 and GAM2920

GR59 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 59(GR59) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR59 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR59 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR59 precursor DNA encodes GR59 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR59 is located from position 6197075 to position 6197181 relative to chromosome 17 on the `-` strand.

GR59 precursor RNA folds spatially, forming GR59 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR59 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR59 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR59 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4027 precursor RNA and GAM6996 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4027 RNA and GAM6996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4027 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4027 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4027 target RNA into GAM4027 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6996 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6996 target RNA into GAM6996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR59 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR59 polynucleotide: GAM4027 target protein and GAM6996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4027 and GAM6996

GR60 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 60(GR60) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR60 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR60 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR60 precursor DNA encodes GR60 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR60 is located from position 40762540 to position 40762622 relative to chromosome 17 on the `-` strand.

GR60 precursor RNA folds spatially, forming GR60 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR60 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR60 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR60 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336731 precursor RNA and GAM336732 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336731 RNA and GAM336732 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336731 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336731 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336731 target RNA into GAM336731 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336732 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336732 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336732 target RNA into GAM336732 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR60 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR60 polynucleotide: GAM336731 target protein and GAM336732 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336731 and GAM336732

GR61 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 61(GR61) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR61 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR61 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR61 precursor DNA encodes GR61 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR61 is located from position 42527933 to position 42528035 relative to chromosome 17 on the `-` strand.

GR61 precursor RNA folds spatially, forming GR61 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR61 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR61 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR61 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336755 precursor RNA and GAM336756 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336755 RNA and GAM336756 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336755 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336755 target RNA into GAM336755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336756 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336756 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336756 target RNA into GAM336756 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR61 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR61 polynucleotide: GAM336755 target protein and GAM336756 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3

TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336755 and GAM336756

GR62 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 62(GR62) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR62 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR62 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR62 precursor DNA encodes GR62 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR62 is located from position 76816688 to position 76816818 relative to chromosome 17 on the `-` strand.

GR62 precursor RNA folds spatially, forming GR62 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR62 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR62 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR62 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2014 precursor RNA and GAM8164 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2014 RNA and GAM8164 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2014 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2014 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2014 target RNA into GAM2014 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8164 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8164 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8164 target RNA into GAM8164 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR62 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR62 polynucleotide: GAM2014 target protein and GAM8164 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM2014 and GAM8164

GR63 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 63(GR63) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR63 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR63 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR63 precursor DNA encodes GR63 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR63 is located from position 182463 to position 182568 relative to chromosome 18 on the `+` strand.

GR63 precursor RNA folds spatially, forming GR63 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR63 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR63 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR63 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4376 precursor RNA and GAM6121 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4376 RNA and GAM6121 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4376 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4376 target RNA into GAM4376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6121 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6121 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6121 target RNA into GAM6121 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR63 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR63 polynucleotide: GAM4376 target protein and GAM6121 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4376 and GAM6121

GR64 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 64(GR64) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR64 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR64 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR64 precursor DNA encodes GR64 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR64 is located from position 37551253 to position 37551384 relative to chromosome 19 on the `+` strand.

GR64 precursor RNA folds spatially, forming GR64 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR64 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR64 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR64 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4796 precursor RNA and GAM5374 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4796 RNA and GAM5374 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4796 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4796 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4796 target RNA into GAM4796 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5374 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5374 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5374 target RNA into GAM5374 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR64 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR64 polynucleotide: GAM4796 target protein and GAM5374 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4796 and GAM5374

GR65 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 65(GR65) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known

in the art.

GR65 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR65 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR65 precursor DNA encodes GR65 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR65 is located from position 43546115 to position 43546218 relative to chromosome 19 on the `+` strand.

GR65 precursor RNA folds spatially, forming GR65 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR65 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR65 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR65 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6055 precursor RNA and GAM7954 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6055 RNA and GAM7954 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6055 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6055 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6055 target RNA into GAM6055 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7954 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7954 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7954 target RNA into GAM7954 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR65 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR65 polynucleotide: GAM6055 target protein and GAM7954 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM6055 and GAM7954

GR66 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 66(GR66) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR66 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR66 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR66 precursor DNA encodes GR66 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR66 is located from position 54394158 to position 54394244 relative to chromosome 19 on the `+` strand.

GR66 precursor RNA folds spatially, forming GR66 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR66 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR66 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR66 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4571 precursor RNA and GAM5008 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4571 RNA and GAM5008 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4571 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated

region of GAM4571 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4571 target RNA into GAM4571 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5008 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5008 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5008 target RNA into GAM5008 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR66 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR66 polynucleotide: GAM4571 target protein and GAM5008 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4571 and GAM5008

GR67 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 67(GR67) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR67 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR67 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR67 precursor DNA encodes GR67 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR67 is located from position 32944216 to position 32944302 relative to chromosome 19 on the `-` strand.

GR67 precursor RNA folds spatially, forming GR67 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR67 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR67 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR67 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA,

is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4189 precursor RNA and GAM5703 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4189 RNA and GAM5703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4189 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4189 target RNA into GAM4189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5703 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5703 target RNA into GAM5703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR67 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR67 polynucleotide: GAM4189 target protein and GAM5703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4189 and GAM5703

GR68 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 68(GR68) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR68 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR68 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR68 precursor DNA encodes GR68 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR68 is located from position 45455573 to position 45455685 relative to chromosome 19 on the `-` strand.

GR68 precursor RNA folds spatially, forming GR68 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR68 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR68 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR68 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336792 precursor RNA and GAM336793 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336792 RNA and GAM336793 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336792 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336792 target RNA into GAM336792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336793 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336793 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336793 target RNA into GAM336793 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR68 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR68 polynucleotide: GAM336792 target protein and GAM336793 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336792 and GAM336793

GR69 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 69(GR69) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR69 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR69 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR69 precursor DNA encodes GR69 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR69 is located from position 74273377 to position 74273476 relative to chromosome 2 on the `+` strand.

GR69 precursor RNA folds spatially, forming GR69 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR69 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR69 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR69 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337146 precursor RNA, GAM337147 precursor RNA and GAM337148 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337146 RNA, GAM337147 RNA and GAM337148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337146 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337146 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337146 target RNA into GAM337146 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337147 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337147 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337147 target RNA into GAM337147 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337148 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337148 target RNA into GAM337148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR69 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR69 polynucleotide: GAM337146 target protein, GAM337147 target protein and GAM337148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337146, GAM337147 and GAM337148

GR70 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 70(GR70) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR70 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR70 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR70 precursor DNA encodes GR70 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR70 is located from position 108115430 to position 108115533 relative to chromosome 2 on the `+` strand.

GR70 precursor RNA folds spatially, forming GR70 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR70 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR70 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR70 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337395 precursor RNA, GAM337396 precursor RNA and GAM337397 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337395 RNA, GAM337396 RNA and GAM337397 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337395 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337395 target RNA into GAM337395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337396 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337396 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337396 target RNA into GAM337396 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337397 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337397 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337397 target RNA into GAM337397 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR70 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR70 polynucleotide: GAM337395 target protein, GAM337396 target protein and GAM337397 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337395, GAM337396 and GAM337397

GR71 Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory polynucleotide, referred to here as Genomic Record 71(GR71) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR71 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR71 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR71 precursor DNA encodes GR71 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR71 is located from position 110164979 to position 110165082 relative to chromosome 2 on the `+` strand.

GR71 precursor RNA folds spatially, forming GR71 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR71 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR71 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR71 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337409 precursor RNA, GAM337410 precursor RNA and GAM337411 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337409 RNA, GAM337410 RNA and GAM337411 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337409 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337409 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337409 target RNA into GAM337409 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337410 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337410 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337410 target RNA into GAM337410 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337411 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337411 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337411 target RNA into GAM337411 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR71 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR71 polynucleotide: GAM337409 target protein, GAM337410 target protein and GAM337411 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337409, GAM337410 and GAM337411

GR72 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 72(GR72) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR72 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR72 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR72 precursor DNA encodes GR72 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR72 is located from position 222613184 to position 222613280 relative to chromosome 2 on the `+` strand.

GR72 precursor RNA folds spatially, forming GR72 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR72 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR72 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR72 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA,

is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337632 precursor RNA and GAM337633 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337632 RNA and GAM337633 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337632 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337632 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337632 target RNA into GAM337632 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337633 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337633 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337633 target RNA into GAM337633 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR72 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR72 polynucleotide: GAM337632 target protein and GAM337633 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337632 and GAM337633

GR73 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 73(GR73) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR73 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR73 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR73 precursor DNA encodes GR73 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR73 is located from position 9554905 to position 9555007 relative to chromosome 2 on the `-` strand.

GR73 precursor RNA folds spatially, forming GR73 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR73 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR73 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR73 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336336 precursor RNA and GAM336337 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336336 RNA and GAM336337 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336336 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336336 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336336 target RNA into GAM336336 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336337 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336337 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336337 target RNA into GAM336337 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR73 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR73 polynucleotide: GAM336336 target protein and GAM336337 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336336 and GAM336337

GR74 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 74(GR74) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR74 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR74 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR74 precursor DNA encodes GR74 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR74 is located from position 106622467 to position 106622570 relative to chromosome 2 on the `-` strand.

GR74 precursor RNA folds spatially, forming GR74 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR74 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR74 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR74 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337385 precursor RNA, GAM337386 precursor RNA and GAM337387 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337385 RNA, GAM337386 RNA and GAM337387 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337385 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337385 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337385 target RNA into GAM337385 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337386 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337386 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337386 target RNA into GAM337386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337387 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337387 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337387 target RNA into GAM337387 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR74 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR74 polynucleotide: GAM337385 target protein, GAM337386 target protein and GAM337387 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337385, GAM337386 and GAM337387

GR75 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 75(GR75) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR75 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR75 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR75 precursor DNA encodes GR75 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR75 is located from position 110894746 to position 110894849 relative to chromosome 2 on the `-` strand.

GR75 precursor RNA folds spatially, forming GR75 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR75 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR75 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR75 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337415 precursor RNA, GAM337416 precursor RNA and GAM337417 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337415 RNA, GAM337416 RNA and GAM337417 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337415 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337415 target RNA into GAM337415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337416 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337416 target RNA into GAM337416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337417 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337417 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337417 target RNA into GAM337417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR75 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR75 polynucleotide: GAM337415 target protein, GAM337416 target protein and GAM337417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337415, GAM337416 and GAM337417

GR76 Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory polynucleotide, referred to here as Genomic Record 76(GR76) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR76 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR76 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR76 precursor DNA encodes GR76 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR76 is located from position 113030916 to position 113031019 relative to chromosome 2 on the `-` strand.

GR76 precursor RNA folds spatially, forming GR76 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR76 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR76 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR76 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337438 precursor RNA, GAM337439 precursor RNA and GAM337440 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337438 RNA, GAM337439 RNA and GAM337440 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337438 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337438 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337438 target RNA into GAM337438 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337439 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337439 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337439 target RNA into GAM337439 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337440 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337440 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337440 target RNA into GAM337440 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR76 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR76 polynucleotide: GAM337438 target protein, GAM337439 target protein and GAM337440 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337438, GAM337439 and GAM337440

GR77 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 77(GR77) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR77 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR77 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR77 precursor DNA encodes GR77 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR77 is located from position 3852982 to position 3853068 relative to chromosome 20 on the `+` strand.

GR77 precursor RNA folds spatially, forming GR77 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR77 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR77 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR77 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA,

is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3266 precursor RNA and GAM5916 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3266 RNA and GAM5916 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3266 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3266 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3266 target RNA into GAM3266 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5916 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5916 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5916 target RNA into GAM5916 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR77 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR77 polynucleotide: GAM3266 target protein and GAM5916 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM3266 and GAM5916

GR78 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 78(GR78) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR78 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR78 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR78 precursor DNA encodes GR78 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR78 is located from position 35736486 to position 35736585 relative to chromosome 20 on the `+` strand.

GR78 precursor RNA folds spatially, forming GR78 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR78 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR78 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR78 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM336661 precursor RNA, GAM336662 precursor RNA, GAM336663 precursor RNA and GAM336664 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336661 RNA, GAM336662 RNA, GAM336663 RNA and GAM336664 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336661 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336661 target RNA into GAM336661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336662 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336662 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336662 target RNA into GAM336662 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336663 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336663 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336663 target RNA into GAM336663 target protein, herein schematically represented by GAM1 TARGET PROTEIN through

GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336664 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336664 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336664 target RNA into GAM336664 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR78 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR78 polynucleotide: GAM336661 target protein, GAM336662 target protein, GAM336663 target protein and GAM336664 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336661, GAM336662, GAM336663 and GAM336664

GR79 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 79(GR79) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR79 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR79 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR79 precursor DNA encodes GR79 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR79 is located from position 46615364 to position 46615468 relative to chromosome 20 on the `-` strand.

GR79 precursor RNA folds spatially, forming GR79 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR79 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR79 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR79 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM750 precursor RNA and GAM1887 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA

segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM750 RNA and GAM1887 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM750 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM750 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM750 target RNA into GAM750 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM1887 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1887 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1887 target RNA into GAM1887 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR79 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR79 polynucleotide: GAM750 target protein and GAM1887 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM750 and GAM1887

GR80 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 80(GR80) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR80 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR80 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR80 precursor DNA encodes GR80 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR80 is located from position 50175599 to position 50175688 relative to chromosome 20 on the `-` strand.

GR80 precursor RNA folds spatially, forming GR80 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR80 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR80 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR80 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2223 precursor RNA and GAM7889 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2223 RNA and GAM7889 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2223 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2223 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2223 target RNA into GAM2223 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7889 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7889 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7889 target RNA into GAM7889 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR80 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR80 polynucleotide: GAM2223 target protein and GAM7889 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM2223 and GAM7889

GR81 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 81(GR81) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like

oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR81 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR81 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR81 precursor DNA encodes GR81 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR81 is located from position 34257285 to position 34257380 relative to chromosome 21 on the `+` strand.

GR81 precursor RNA folds spatially, forming GR81 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR81 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR81 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR81 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336642 precursor RNA and GAM336643 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336642 RNA and GAM336643 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336642 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336642 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336642 target RNA into GAM336642 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336643 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336643 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336643 target RNA into GAM336643

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR81 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR81 polynucleotide: GAM336642 target protein and GAM336643 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336642 and GAM336643

GR82 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 82(GR82) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR82 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR82 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR82 precursor DNA encodes GR82 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR82 is located from position 48973458 to position 48973552 relative to chromosome 22 on the `+` strand.

GR82 precursor RNA folds spatially, forming GR82 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR82 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR82 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR82 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336844 precursor RNA and GAM336845 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336844 RNA and GAM336845 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336844 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336844 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336844 target RNA into GAM336844 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336845 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336845 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336845 target RNA into GAM336845 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR82 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR82 polynucleotide: GAM336844 target protein and GAM336845 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336844 and GAM336845

GR83 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 83(GR83) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR83 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR83 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR83 precursor DNA encodes GR83 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR83 is located from position 22354493 to position 22354606 relative to chromosome 22 on the `-` strand.

GR83 precursor RNA folds spatially, forming GR83 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR83 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR83 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR83 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2300 precursor RNA and GAM2391 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2300 RNA and GAM2391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2300 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2300 target RNA into GAM2300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2391 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2391 target RNA into GAM2391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR83 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR83 polynucleotide: GAM2300 target protein and GAM2391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM2300 and GAM2391

GR84 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 84(GR84) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR84 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR84 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR84 precursor DNA encodes GR84 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR84 is located from position 44721785 to position 44721915 relative to chromosome 22 on the `-` strand.

GR84 precursor RNA folds spatially, forming GR84 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR84 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR84 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR84 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1479 precursor RNA and GAM6982 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1479 RNA and GAM6982 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1479 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1479 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1479 target RNA into GAM1479 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6982 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6982 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6982 target RNA into GAM6982 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR84 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR84 polynucleotide: GAM1479 target protein and GAM6982 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3

TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1479 and GAM6982

GR85 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 85(GR85) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR85 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR85 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR85 precursor DNA encodes GR85 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR85 is located from position 89368234 to position 89368332 relative to chromosome 4 on the `+` strand.

GR85 precursor RNA folds spatially, forming GR85 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR85 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR85 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR85 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337237 precursor RNA and GAM337238 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337237 RNA and GAM337238 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337237 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337237 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337237 target RNA into GAM337237 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337238 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337238 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337238 target RNA into GAM337238 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR85 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR85 polynucleotide: GAM337237 target protein and GAM337238 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337237 and GAM337238

GR86 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 86(GR86) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR86 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR86 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR86 precursor DNA encodes GR86 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR86 is located from position 17062066 to position 17062152 relative to chromosome 7 on the `+` strand.

GR86 precursor RNA folds spatially, forming GR86 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR86 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR86 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR86 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336432 precursor RNA and GAM336433 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336432 RNA and GAM336433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336432 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336432 target RNA into GAM336432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336433 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336433 target RNA into GAM336433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR86 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR86 polynucleotide: GAM336432 target protein and GAM336433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336432 and GAM336433

GR87 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 87(GR87) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR87 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR87 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR87 precursor DNA encodes GR87 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR87 is located from position 82179625 to position 82179721 relative to chromosome 7 on the `-` strand.

GR87 precursor RNA folds spatially, forming GR87 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR87 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR87 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR87 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1088 precursor RNA and GAM7250 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1088 RNA and GAM7250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1088 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1088 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1088 target RNA into GAM1088 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7250 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7250 target RNA into GAM7250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR87 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR87 polynucleotide: GAM1088 target protein and GAM7250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1088 and GAM7250

GR88 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 88(GR88) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known

in the art.

GR88 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR88 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR88 precursor DNA encodes GR88 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR88 is located from position 137087025 to position 137087139 relative to chromosome 7 on the `-` strand.

GR88 precursor RNA folds spatially, forming GR88 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR88 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR88 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR88 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337570 precursor RNA, GAM337571 precursor RNA and GAM337572 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337570 RNA, GAM337571 RNA and GAM337572 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337570 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337570 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337570 target RNA into GAM337570 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337571 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337571 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337571 target RNA into GAM337571 target protein, herein schematically represented by GAM1 TARGET PROTEIN through

GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337572 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337572 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337572 target RNA into GAM337572 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR88 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR88 polynucleotide: GAM337570 target protein, GAM337571 target protein and GAM337572 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337570, GAM337571 and GAM337572

GR89 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 89(GR89) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR89 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR89 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR89 precursor DNA encodes GR89 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR89 is located from position 140693627 to position 140693723 relative to chromosome 7 on the `-` strand.

GR89 precursor RNA folds spatially, forming GR89 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR89 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR89 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR89 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6618 precursor RNA and GAM6978 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA

segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6618 RNA and GAM6978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6618 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6618 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6618 target RNA into GAM6618 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6978 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6978 target RNA into GAM6978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR89 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR89 polynucleotide: GAM6618 target protein and GAM6978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM6618 and GAM6978

GR90 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 90(GR90) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR90 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR90 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR90 precursor DNA encodes GR90 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR90 is located from position 148136535 to position 148136637 relative to chromosome 7 on the `-` strand.

GR90 precursor RNA folds spatially, forming GR90 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR90 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR90 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR90 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337597 precursor RNA and GAM337598 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337597 RNA and GAM337598 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337597 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337597 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337597 target RNA into GAM337597 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337598 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337598 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337598 target RNA into GAM337598 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR90 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR90 polynucleotide: GAM337597 target protein and GAM337598 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337597 and GAM337598

GR91 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 91(GR91) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like

oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR91 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR91 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR91 precursor DNA encodes GR91 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR91 is located from position 150223532 to position 150223641 relative to chromosome 7 on the `-` strand.

GR91 precursor RNA folds spatially, forming GR91 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR91 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR91 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR91 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM193 precursor RNA and GAM973 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM193 RNA and GAM973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM193 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM193 target RNA into GAM193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM973 target RNA into GAM973 target

protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR91 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR91 polynucleotide: GAM193 target protein and GAM973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM193 and GAM973

GR92 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 92(GR92) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR92 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR92 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR92 precursor DNA encodes GR92 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR92 is located from position 30119301 to position 30119415 relative to chromosome 8 on the `+` strand.

GR92 precursor RNA folds spatially, forming GR92 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR92 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR92 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR92 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336595 precursor RNA and GAM336596 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336595 RNA and GAM336596 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336595 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336595 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336595 target RNA into GAM336595 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336596 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336596 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336596 target RNA into GAM336596 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR92 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR92 polynucleotide: GAM336595 target protein and GAM336596 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336595 and GAM336596

GR93 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 93(GR93) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR93 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR93 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR93 precursor DNA encodes GR93 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR93 is located from position 33338251 to position 33338352 relative to chromosome 9 on the `+` strand.

GR93 precursor RNA folds spatially, forming GR93 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR93 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR93 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR93 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336630 precursor RNA and GAM336631 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336630 RNA and GAM336631 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336630 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336630 target RNA into GAM336630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336631 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336631 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336631 target RNA into GAM336631 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR93 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR93 polynucleotide: GAM336630 target protein and GAM336631 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336630 and GAM336631

GR94 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 94(GR94) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR94 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR94 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR94 precursor DNA encodes GR94 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR94 is located from position 35798279 to position 35798393 relative to chromosome 9 on the `+` strand.

GR94 precursor RNA folds spatially, forming GR94 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR94 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR94 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR94 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1550 precursor RNA and GAM1937 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1550 RNA and GAM1937 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1550 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1550 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1550 target RNA into GAM1550 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM1937 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1937 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1937 target RNA into GAM1937 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR94 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR94 polynucleotide: GAM1550 target protein and GAM1937 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3

TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1550 and GAM1937

GR95 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 95(GR95) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR95 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR95 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR95 precursor DNA encodes GR95 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR95 is located from position 68096932 to position 68097040 relative to chromosome 9 on the `+` strand.

GR95 precursor RNA folds spatially, forming GR95 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR95 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR95 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR95 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337051 precursor RNA and GAM337052 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337051 RNA and GAM337052 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337051 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337051 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337051 target RNA into GAM337051 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337052 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337052 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337052 target RNA into GAM337052 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR95 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR95 polynucleotide: GAM337051 target protein and GAM337052 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337051 and GAM337052

GR96 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 96(GR96) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR96 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR96 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR96 precursor DNA encodes GR96 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR96 is located from position 97689214 to position 97691182 relative to chromosome 9 on the `+` strand.

GR96 precursor RNA folds spatially, forming GR96 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR96 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR96 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR96 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM259 precursor RNA, GAM1423 precursor RNA, GAM4709 precursor RNA and GAM7363 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM259 RNA, GAM1423 RNA, GAM4709 RNA and GAM7363 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM259 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM259 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM259 target RNA into GAM259 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM1423 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1423 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1423 target RNA into GAM1423 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4709 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4709 target RNA into GAM4709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7363 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7363 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7363 target RNA into GAM7363 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR96 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR96 polynucleotide: GAM259 target protein, GAM1423 target protein, GAM4709 target protein and GAM7363 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM259, GAM1423, GAM4709 and GAM7363

GR97 Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory polynucleotide, referred to here as Genomic Record 97(GR97) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR97 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR97 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR97 precursor DNA encodes GR97 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR97 is located from position 128399235 to position 128399347 relative to chromosome 9 on the `+` strand.

GR97 precursor RNA folds spatially, forming GR97 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR97 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR97 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR97 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337521 precursor RNA, GAM337522 precursor RNA and GAM337523 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337521 RNA, GAM337522 RNA and GAM337523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337521 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337521 target RNA into GAM337521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337522 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337522 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337522 target RNA into GAM337522 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337523 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337523 target RNA into GAM337523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR97 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR97 polynucleotide: GAM337521 target protein, GAM337522 target protein and GAM337523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337521, GAM337522 and GAM337523

GR98 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 98(GR98) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR98 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR98 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR98 precursor DNA encodes GR98 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR98 is located from position 43025631 to position 43025765 relative to chromosome 9 on the `-` strand.

GR98 precursor RNA folds spatially, forming GR98 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR98 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR98 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR98 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA,

is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4986 precursor RNA, GAM5085 precursor RNA and GAM7017 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4986 RNA, GAM5085 RNA and GAM7017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4986 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4986 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4986 target RNA into GAM4986 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5085 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5085 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5085 target RNA into GAM5085 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7017 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7017 target RNA into GAM7017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR98 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR98 polynucleotide: GAM4986 target protein, GAM5085 target protein and GAM7017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4986, GAM5085 and GAM7017

GR99 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 99(GR99) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR99 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR99 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR99 precursor DNA encodes GR99 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR99 is located from position 62131098 to position 62131226 relative to chromosome 9 on the `-` strand.

GR99 precursor RNA folds spatially, forming GR99 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR99 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR99 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR99 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2272 precursor RNA, GAM5764 precursor RNA and GAM7345 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2272 RNA, GAM5764 RNA and GAM7345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2272 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2272 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2272 target RNA into GAM2272 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5764 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5764 target RNA into GAM5764 target

protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7345 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7345 target RNA into GAM7345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR99 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR99 polynucleotide: GAM2272 target protein, GAM5764 target protein and GAM7345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM2272, GAM5764 and GAM7345

GR100 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 100(GR100) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR100 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR100 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR100 precursor DNA encodes GR100 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR100 is located from position 62875338 to position 62875466 relative to chromosome 9 on the `-` strand.

GR100 precursor RNA folds spatially, forming GR100 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR100 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR100 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR100 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM336978 precursor RNA, GAM336980 precursor RNA and GAM336981 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs

being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336978 RNA, GAM336980 RNA and GAM336981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336978 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336978 target RNA into GAM336978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336980 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336980 target RNA into GAM336980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336981 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336981 target RNA into GAM336981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR100 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR100 polynucleotide: GAM336978 target protein, GAM336980 target protein and GAM336981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336978, GAM336980 and GAM336981

GR101 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 101(GR101) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR101 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR101 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR101 precursor DNA encodes GR101 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR101 is located from position 116757828 to position 116757946 relative to chromosome 9 on the `-` strand.

GR101 precursor RNA folds spatially, forming GR101 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR101 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR101 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR101 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4932 precursor RNA, GAM6024 precursor RNA and GAM6417 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4932 RNA, GAM6024 RNA and GAM6417 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4932 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4932 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4932 target RNA into GAM4932 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6024 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6024 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6024 target RNA into GAM6024 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6417 RNA, herein schematically represented by GAM1 RNA through GAM3

RNA, binds complementarily to a target binding site located in an untranslated region of GAM6417 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6417 target RNA into GAM6417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR101 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR101 polynucleotide: GAM4932 target protein, GAM6024 target protein and GAM6417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4932, GAM6024 and GAM6417

GR102 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 102(GR102) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR102 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR102 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR102 precursor DNA encodes GR102 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR102 is located from position 124608557 to position 124608671 relative to chromosome 9 on the `-` strand.

GR102 precursor RNA folds spatially, forming GR102 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR102 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR102 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR102 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM337498 precursor RNA, GAM337499 precursor RNA, GAM337500 precursor RNA and GAM337501 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337498 RNA, GAM337499 RNA, GAM337500 RNA and GAM337501 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337498 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337498 target RNA into GAM337498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337499 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337499 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337499 target RNA into GAM337499 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337500 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337500 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337500 target RNA into GAM337500 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337501 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337501 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337501 target RNA into GAM337501 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR102 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR102 polynucleotide: GAM337498 target protein, GAM337499 target protein, GAM337500 target protein and GAM337501 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337498, GAM337499, GAM337500 and GAM337501

GR103 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 103(GR103)

polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR103 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR103 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR103 precursor DNA encodes GR103 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR103 is located from position 120997503 to position 120997605 relative to chromosome X on the `+` strand.

GR103 precursor RNA folds spatially, forming GR103 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR103 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR103 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR103 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7776 precursor RNA and GAM337476 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7776 RNA and GAM337476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7776 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7776 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7776 target RNA into GAM7776 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig. 8, thereby inhibiting translation of GAM337476 target RNA into GAM337476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR103 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR103 polynucleotide: GAM7776 target protein and GAM337476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM7776 and GAM337476

GR104 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 104(GR104) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR104 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR104 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR104 precursor DNA encodes GR104 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR104 is located from position 136594068 to position 136594193 relative to chromosome X on the `+` strand.

GR104 precursor RNA folds spatially, forming GR104 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR104 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR104 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR104 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1782 precursor RNA, GAM8047 precursor RNA and GAM8349 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1782 RNA, GAM8047 RNA and GAM8349 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to

GAM RNA of Fig. 8.

GAM1782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1782 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1782 target RNA into GAM1782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8047 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8047 target RNA into GAM8047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8349 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8349 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8349 target RNA into GAM8349 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR104 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR104 polynucleotide: GAM1782 target protein, GAM8047 target protein and GAM8349 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1782, GAM8047 and GAM8349

GR105 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 105(GR105) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR105 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR105 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR105 precursor DNA encodes GR105 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR105 is located from position 7772009

to position 7772133 relative to chromosome X on the `-` strand.

GR105 precursor RNA folds spatially, forming GR105 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR105 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR105 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR105 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5673 precursor RNA and GAM5823 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5673 RNA and GAM5823 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5673 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5673 target RNA into GAM5673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5823 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5823 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5823 target RNA into GAM5823 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR105 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR105 polynucleotide: GAM5673 target protein and GAM5823 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM5673 and GAM5823

GR106 Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory polynucleotide, referred to here as Genomic Record 106(GR106) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR106 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR106 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR106 precursor DNA encodes GR106 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR106 is located from position 23528432 to position 23528526 relative to chromosome X on the `-` strand.

GR106 precursor RNA folds spatially, forming GR106 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR106 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR106 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR106 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336526 precursor RNA and GAM336527 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336526 RNA and GAM336527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336526 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336526 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336526 target RNA into GAM336526 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336527 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to

a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336527 target RNA into GAM336527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR106 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR106 polynucleotide: GAM336526 target protein and GAM336527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336526 and GAM336527

GR107 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 107(GR107) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR107 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR107 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR107 precursor DNA encodes GR107 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR107 is located from position 47741101 to position 47741216 relative to chromosome X on the `-` strand.

GR107 precursor RNA folds spatially, forming GR107 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR107 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR107 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR107 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7022 precursor RNA and GAM7135 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7022 RNA and GAM7135 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig.

8.

GAM7022 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7022 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7022 target RNA into GAM7022 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7135 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7135 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7135 target RNA into GAM7135 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR107 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR107 polynucleotide: GAM7022 target protein and GAM7135 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM7022 and GAM7135

GR108 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 108(GR108) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR108 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR108 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR108 precursor DNA encodes GR108 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR108 is located from position 47783494 to position 47783586 relative to chromosome X on the `-` strand.

GR108 precursor RNA folds spatially, forming GR108 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR108 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR108 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a

partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR108 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336825 precursor RNA and GAM336826 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336825 RNA and GAM336826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336825 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336825 target RNA into GAM336825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336826 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336826 target RNA into GAM336826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR108 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR108 polynucleotide: GAM336825 target protein and GAM336826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336825 and GAM336826

GR109 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 109(GR109) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR109 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The

method by which GR109 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR109 precursor DNA encodes GR109 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR109 is located from position 126882804 to position 126883120 relative to chromosome X on the `-` strand.

GR109 precursor RNA folds spatially, forming GR109 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR109 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR109 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR109 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1033 precursor RNA and GAM5963 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1033 RNA and GAM5963 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1033 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1033 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1033 target RNA into GAM1033 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5963 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5963 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5963 target RNA into GAM5963 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR109 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like`

cluster of GR109 polynucleotide: GAM1033 target protein and GAM5963 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1033 and GAM5963

GR111 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 111(GR111) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR111 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR111 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR111 precursor DNA encodes GR111 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR111 is located from position 11686899 to position 11687001 relative to chromosome 1 on the `-` strand.

GR111 precursor RNA folds spatially, forming GR111 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR111 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR111 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR111 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336373 precursor RNA and GAM336374 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336373 RNA and GAM336374 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336373 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336373 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336373 target RNA into GAM336373

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336374 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336374 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336374 target RNA into GAM336374 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR111 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR111 polynucleotide: GAM336373 target protein and GAM336374 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336373 and GAM336374

GR112 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 112(GR112) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR112 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR112 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR112 precursor DNA encodes GR112 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR112 is located from position 116189890 to position 116189992 relative to chromosome 1 on the `-` strand.

GR112 precursor RNA folds spatially, forming GR112 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR112 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR112 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR112 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337453 precursor RNA and GAM337454 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA

segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337453 RNA and GAM337454 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337453 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337453 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337453 target RNA into GAM337453 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337454 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337454 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337454 target RNA into GAM337454 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR112 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR112 polynucleotide: GAM337453 target protein and GAM337454 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337453 and GAM337454

GR113 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 113(GR113) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR113 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR113 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR113 precursor DNA encodes GR113 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR113 is located from position 43586567 to position 43586676 relative to chromosome 13 on the `+` strand.

GR113 precursor RNA folds spatially, forming GR113 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR113 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR113 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR113 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336770 precursor RNA and GAM336771 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336770 RNA and GAM336771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336770 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336770 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336770 target RNA into GAM336770 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336771 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336771 target RNA into GAM336771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR113 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR113 polynucleotide: GAM336770 target protein and GAM336771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336770 and GAM336771

GR114 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 114(GR114) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like

oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR114 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR114 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR114 precursor DNA encodes GR114 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR114 is located from position 30643328 to position 30643430 relative to chromosome 16 on the `+` strand.

GR114 precursor RNA folds spatially, forming GR114 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR114 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR114 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR114 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336599 precursor RNA and GAM336600 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336599 RNA and GAM336600 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336599 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336599 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336599 target RNA into GAM336599 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336600 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336600 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336600 target RNA into GAM336600

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR114 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR114 polynucleotide: GAM336599 target protein and GAM336600 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336599 and GAM336600

GR115 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 115(GR115) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR115 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR115 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR115 precursor DNA encodes GR115 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR115 is located from position 47935242 to position 47935318 relative to chromosome 17 on the `+` strand.

GR115 precursor RNA folds spatially, forming GR115 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR115 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR115 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR115 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336827 precursor RNA and GAM336828 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336827 RNA and GAM336828 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336827 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336827 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336827 target RNA into GAM336827 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336828 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336828 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336828 target RNA into GAM336828 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR115 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR115 polynucleotide: GAM336827 target protein and GAM336828 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336827 and GAM336828

GR116 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 116(GR116) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR116 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR116 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR116 precursor DNA encodes GR116 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR116 is located from position 63490699 to position 63490788 relative to chromosome 19 on the `+` strand.

GR116 precursor RNA folds spatially, forming GR116 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR116 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR116 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR116 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336995 precursor RNA and GAM336996 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336995 RNA and GAM336996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336995 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336995 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336995 target RNA into GAM336995 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336996 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336996 target RNA into GAM336996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR116 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR116 polynucleotide: GAM336995 target protein and GAM336996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336995 and GAM336996

GR117 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 117(GR117) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR117 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR117 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR117 precursor DNA encodes GR117 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR117 is located from position 12791804 to position 12791905 relative to chromosome 19 on the `-` strand.

GR117 precursor RNA folds spatially, forming GR117 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR117 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR117 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR117 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM336390 precursor RNA, GAM336391 precursor RNA and GAM336392 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336390 RNA, GAM336391 RNA and GAM336392 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336390 target RNA into GAM336390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336391 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336391 target RNA into GAM336391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336392 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336392 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig. 8, thereby inhibiting translation of GAM336392 target RNA into GAM336392 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR117 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR117 polynucleotide: GAM336390 target protein, GAM336391 target protein and GAM336392 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336390, GAM336391 and GAM336392

GR118 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 118(GR118) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR118 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR118 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR118 precursor DNA encodes GR118 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR118 is located from position 101642187 to position 101642300 relative to chromosome 7 on the `+` strand.

GR118 precursor RNA folds spatially, forming GR118 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR118 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR118 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR118 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337350 precursor RNA, GAM337351 precursor RNA and GAM337352 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337350 RNA, GAM337351 RNA and GAM337352 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337350 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337350 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337350 target RNA into GAM337350 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337351 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337351 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337351 target RNA into GAM337351 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337352 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337352 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337352 target RNA into GAM337352 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR118 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR118 polynucleotide: GAM337350 target protein, GAM337351 target protein and GAM337352 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337350, GAM337351 and GAM337352

GR119 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 119(GR119) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR119 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR119 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR119 precursor DNA encodes GR119 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR119 is located from position 65582433 to position 65582810 relative to chromosome 9 on the `+` strand.

GR119 precursor RNA folds spatially, forming GR119 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR119 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR119 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR119 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337016 precursor RNA and GAM337017 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337016 RNA and GAM337017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337016 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337016 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337016 target RNA into GAM337016 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337017 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337017 target RNA into GAM337017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR119 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR119 polynucleotide: GAM337016 target protein and GAM337017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337016 and GAM337017

GR122 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 122(GR122) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR122 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR122 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR122 precursor DNA encodes GR122 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR122 is located from position 151095622 to position 151095721 relative to chromosome 1 on the `+` strand.

GR122 precursor RNA folds spatially, forming GR122 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR122 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR122 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR122 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337607 precursor RNA and GAM337608 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337607 RNA and GAM337608 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337607 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337607 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337607 target RNA into GAM337607 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337608 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM337608 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337608 target RNA into GAM337608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR122 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR122 polynucleotide: GAM337607 target protein and GAM337608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337607 and GAM337608

GR123 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 123(GR123) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR123 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR123 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR123 precursor DNA encodes GR123 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR123 is located from position 6079591 to position 6079695 relative to chromosome 10 on the `+` strand.

GR123 precursor RNA folds spatially, forming GR123 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR123 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR123 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR123 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336297 precursor RNA and GAM336298 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides

in length, GAM336297 RNA and GAM336298 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336297 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336297 target RNA into GAM336297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336298 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336298 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336298 target RNA into GAM336298 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR123 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR123 polynucleotide: GAM336297 target protein and GAM336298 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336297 and GAM336298

GR124 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 124(GR124) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR124 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR124 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR124 precursor DNA encodes GR124 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR124 is located from position 74733011 to position 74733112 relative to chromosome 10 on the `+` strand.

GR124 precursor RNA folds spatially, forming GR124 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR124 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the

nucleotide sequence of GR124 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR124 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337154 precursor RNA, GAM337155 precursor RNA and GAM337156 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337154 RNA, GAM337155 RNA and GAM337156 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337154 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337154 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337154 target RNA into GAM337154 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337155 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337155 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337155 target RNA into GAM337155 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337156 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337156 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337156 target RNA into GAM337156 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR124 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR124 polynucleotide: GAM337154 target protein, GAM337155 target protein and GAM337156 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is

elaborated in Table 8, with references to GAM337154, GAM337155 and GAM337156

GR125 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 125(GR125) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR125 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR125 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR125 precursor DNA encodes GR125 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR125 is located from position 79169031 to position 79169147 relative to chromosome 10 on the `+` strand.

GR125 precursor RNA folds spatially, forming GR125 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR125 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR125 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR125 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1443 precursor RNA and GAM5728 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1443 RNA and GAM5728 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1443 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1443 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1443 target RNA into GAM1443 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5728 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5728 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5728 target RNA into GAM5728 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR125 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR125 polynucleotide: GAM1443 target protein and GAM5728 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1443 and GAM5728

GR126 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 126(GR126) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR126 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR126 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR126 precursor DNA encodes GR126 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR126 is located from position 92938874 to position 92938984 relative to chromosome 10 on the `+` strand.

GR126 precursor RNA folds spatially, forming GR126 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR126 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR126 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR126 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337257 precursor RNA and GAM337258 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337257 RNA and GAM337258 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337257 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337257 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337257 target RNA into GAM337257 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337258 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337258 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337258 target RNA into GAM337258 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR126 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR126 polynucleotide: GAM337257 target protein and GAM337258 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337257 and GAM337258

GR127 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 127(GR127) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR127 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR127 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR127 precursor DNA encodes GR127 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR127 is located from position 95469300 to position 95469401 relative to chromosome 10 on the `+` strand.

GR127 precursor RNA folds spatially, forming GR127 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR127

folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR127 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR127 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337281 precursor RNA and GAM337282 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337281 RNA and GAM337282 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337281 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337281 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337281 target RNA into GAM337281 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337282 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337282 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337282 target RNA into GAM337282 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR127 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR127 polynucleotide: GAM337281 target protein and GAM337282 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337281 and GAM337282

GR128 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 128(GR128) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known

in the art.

GR128 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR128 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR128 precursor DNA encodes GR128 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR128 is located from position 98645765 to position 98645837 relative to chromosome 10 on the `+` strand.

GR128 precursor RNA folds spatially, forming GR128 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR128 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR128 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR128 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337305 precursor RNA and GAM337306 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337305 RNA and GAM337306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337305 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337305 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337305 target RNA into GAM337305 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337306 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337306 target RNA into GAM337306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR128 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR128 polynucleotide: GAM337305 target protein and GAM337306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337305 and GAM337306

GR129 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 129(GR129) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR129 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR129 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR129 precursor DNA encodes GR129 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR129 is located from position 130940694 to position 130940793 relative to chromosome 10 on the `+` strand.

GR129 precursor RNA folds spatially, forming GR129 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR129 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR129 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR129 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337541 precursor RNA and GAM337542 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337541 RNA and GAM337542 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM337541 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337541 target RNA into GAM337541 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337542 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337542 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337542 target RNA into GAM337542 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR129 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR129 polynucleotide: GAM337541 target protein and GAM337542 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337541 and GAM337542

GR130 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 130(GR130) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR130 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR130 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR130 precursor DNA encodes GR130 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR130 is located from position 36386596 to position 36386704 relative to chromosome 10 on the `-` strand.

GR130 precursor RNA folds spatially, forming GR130 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR130 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR130 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR130 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA,

is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM336670 precursor RNA, GAM336671 precursor RNA and GAM336672 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336670 RNA, GAM336671 RNA and GAM336672 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336670 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336670 target RNA into GAM336670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336671 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336671 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336671 target RNA into GAM336671 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336672 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336672 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336672 target RNA into GAM336672 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR130 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR130 polynucleotide: GAM336670 target protein, GAM336671 target protein and GAM336672 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336670, GAM336671 and GAM336672

GR131 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 131(GR131) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like

oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR131 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR131 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR131 precursor DNA encodes GR131 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR131 is located from position 5537268 to position 5537355 relative to chromosome 11 on the `+` strand.

GR131 precursor RNA folds spatially, forming GR131 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR131 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR131 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR131 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336289 precursor RNA and GAM336290 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336289 RNA and GAM336290 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336289 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336289 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336289 target RNA into GAM336289 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336290 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336290 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336290 target RNA into GAM336290

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR131 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR131 polynucleotide: GAM336289 target protein and GAM336290 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336289 and GAM336290

GR132 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 132(GR132) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR132 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR132 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR132 precursor DNA encodes GR132 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR132 is located from position 9504192 to position 9504294 relative to chromosome 11 on the `+` strand.

GR132 precursor RNA folds spatially, forming GR132 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR132 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR132 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR132 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336334 precursor RNA and GAM336335 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336334 RNA and GAM336335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336334 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336334 target RNA into GAM336334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336335 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336335 target RNA into GAM336335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR132 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR132 polynucleotide: GAM336334 target protein and GAM336335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336334 and GAM336335

GR133 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 133(GR133) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR133 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR133 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR133 precursor DNA encodes GR133 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR133 is located from position 18148992 to position 18149072 relative to chromosome 11 on the `+` strand.

GR133 precursor RNA folds spatially, forming GR133 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR133 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR133 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR133 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336439 precursor RNA and GAM336440 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336439 RNA and GAM336440 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336439 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336439 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336439 target RNA into GAM336439 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336440 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336440 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336440 target RNA into GAM336440 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR133 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR133 polynucleotide: GAM336439 target protein and GAM336440 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336439 and GAM336440

GR134 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 134(GR134) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR134 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR134 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR134 precursor DNA encodes GR134 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR134 is located from position 68013714 to position 68013821 relative to chromosome 11 on the `+` strand.

GR134 precursor RNA folds spatially, forming GR134 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR134 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR134 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR134 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3195 precursor RNA and GAM7845 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3195 RNA and GAM7845 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3195 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3195 target RNA into GAM3195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7845 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7845 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7845 target RNA into GAM7845 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR134 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR134 polynucleotide: GAM3195 target protein and GAM7845 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3

TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM3195 and GAM7845

GR135 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 135(GR135) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR135 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR135 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR135 precursor DNA encodes GR135 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR135 is located from position 88200943 to position 88201073 relative to chromosome 11 on the `+` strand.

GR135 precursor RNA folds spatially, forming GR135 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR135 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR135 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR135 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6567 precursor RNA and GAM8539 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6567 RNA and GAM8539 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6567 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6567 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6567 target RNA into GAM6567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8539 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8539 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8539 target RNA into GAM8539 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR135 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR135 polynucleotide: GAM6567 target protein and GAM8539 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM6567 and GAM8539

GR136 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 136(GR136) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR136 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR136 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR136 precursor DNA encodes GR136 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR136 is located from position 90083877 to position 90083973 relative to chromosome 11 on the `+` strand.

GR136 precursor RNA folds spatially, forming GR136 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR136 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR136 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR136 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337245 precursor RNA and GAM337246 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337245 RNA and GAM337246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337245 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337245 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337245 target RNA into GAM337245 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337246 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337246 target RNA into GAM337246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR136 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR136 polynucleotide: GAM337245 target protein and GAM337246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337245 and GAM337246

GR137 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 137(GR137) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR137 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR137 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR137 precursor DNA encodes GR137 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR137 is located from position 99654607 to position 99654738 relative to chromosome 11 on the `+` strand.

GR137 precursor RNA folds spatially, forming GR137 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR137

folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR137 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR137 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337326 precursor RNA, GAM337327 precursor RNA and GAM337328 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337326 RNA, GAM337327 RNA and GAM337328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337326 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337326 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337326 target RNA into GAM337326 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337327 target RNA into GAM337327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337328 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337328 target RNA into GAM337328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR137 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR137 polynucleotide: GAM337326 target protein, GAM337327 target

protein and GAM337328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337326, GAM337327 and GAM337328

GR138 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 138(GR138) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR138 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR138 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR138 precursor DNA encodes GR138 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR138 is located from position 111702787 to position 111702870 relative to chromosome 11 on the `+` strand.

GR138 precursor RNA folds spatially, forming GR138 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR138 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR138 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR138 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337424 precursor RNA and GAM337425 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337424 RNA and GAM337425 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337424 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337424 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337424 target RNA into GAM337424

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337425 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337425 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337425 target RNA into GAM337425 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR138 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR138 polynucleotide: GAM337424 target protein and GAM337425 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337424 and GAM337425

GR139 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 139(GR139) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR139 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR139 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR139 precursor DNA encodes GR139 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR139 is located from position 113971966 to position 113972054 relative to chromosome 11 on the `+` strand.

GR139 precursor RNA folds spatially, forming GR139 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR139 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR139 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR139 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4188 precursor RNA and GAM5623 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA

segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4188 RNA and GAM5623 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4188 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4188 target RNA into GAM4188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5623 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5623 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5623 target RNA into GAM5623 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR139 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR139 polynucleotide: GAM4188 target protein and GAM5623 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4188 and GAM5623

GR140 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 140(GR140) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR140 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR140 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR140 precursor DNA encodes GR140 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR140 is located from position 126234545 to position 126234647 relative to chromosome 11 on the `+` strand.

GR140 precursor RNA folds spatially, forming GR140 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR140 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR140 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR140 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337507 precursor RNA and GAM337508 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337507 RNA and GAM337508 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337507 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337507 target RNA into GAM337507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337508 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337508 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337508 target RNA into GAM337508 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR140 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR140 polynucleotide: GAM337507 target protein and GAM337508 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337507 and GAM337508

GR141 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 141(GR141) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like

oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR141 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR141 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR141 precursor DNA encodes GR141 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR141 is located from position 46654581 to position 46654675 relative to chromosome 11 on the `-` strand.

GR141 precursor RNA folds spatially, forming GR141 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR141 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR141 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR141 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336810 precursor RNA and GAM336811 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336810 RNA and GAM336811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336810 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336810 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336810 target RNA into GAM336810 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336811 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336811 target RNA into GAM336811

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR141 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR141 polynucleotide: GAM336810 target protein and GAM336811 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336810 and GAM336811

GR142 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 142(GR142) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR142 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR142 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR142 precursor DNA encodes GR142 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR142 is located from position 50911119 to position 50911225 relative to chromosome 12 on the `+` strand.

GR142 precursor RNA folds spatially, forming GR142 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR142 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR142 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR142 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336876 precursor RNA and GAM336877 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336876 RNA and GAM336877 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336876 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336876 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336876 target RNA into GAM336876 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336877 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336877 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336877 target RNA into GAM336877 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR142 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR142 polynucleotide: GAM336876 target protein and GAM336877 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336876 and GAM336877

GR143 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 143(GR143) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR143 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR143 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR143 precursor DNA encodes GR143 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR143 is located from position 57533860 to position 57533948 relative to chromosome 12 on the `+` strand.

GR143 precursor RNA folds spatially, forming GR143 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR143 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR143 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR143 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336925 precursor RNA and GAM336926 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336925 RNA and GAM336926 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336925 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336925 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336925 target RNA into GAM336925 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336926 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336926 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336926 target RNA into GAM336926 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR143 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR143 polynucleotide: GAM336925 target protein and GAM336926 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336925 and GAM336926

GR144 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 144(GR144) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR144 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR144 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR144 precursor DNA encodes GR144 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR144 is located from position 62689480 to position 62689572 relative to chromosome 12 on the `+` strand.

GR144 precursor RNA folds spatially, forming GR144 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR144 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR144 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR144 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336970 precursor RNA and GAM336971 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336970 RNA and GAM336971 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336970 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336970 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336970 target RNA into GAM336970 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336971 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336971 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336971 target RNA into GAM336971 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR144 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR144 polynucleotide: GAM336970 target protein and GAM336971 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3

TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336970 and GAM336971

GR145 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 145(GR145) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR145 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR145 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR145 precursor DNA encodes GR145 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR145 is located from position 66457769 to position 66457886 relative to chromosome 12 on the `+` strand.

GR145 precursor RNA folds spatially, forming GR145 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR145 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR145 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR145 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337032 precursor RNA and GAM337033 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337032 RNA and GAM337033 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337032 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337032 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337032 target RNA into GAM337032 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337033 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337033 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337033 target RNA into GAM337033 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR145 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR145 polynucleotide: GAM337032 target protein and GAM337033 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337032 and GAM337033

GR146 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 146(GR146) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR146 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR146 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR146 precursor DNA encodes GR146 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR146 is located from position 85256084 to position 85256183 relative to chromosome 12 on the `+` strand.

GR146 precursor RNA folds spatially, forming GR146 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR146 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR146 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR146 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337213 precursor RNA, GAM337214 precursor RNA and GAM337215 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337213 RNA, GAM337214 RNA and GAM337215 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337213 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337213 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337213 target RNA into GAM337213 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337214 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337214 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337214 target RNA into GAM337214 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337215 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337215 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337215 target RNA into GAM337215 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR146 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR146 polynucleotide: GAM337213 target protein, GAM337214 target protein and GAM337215 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337213, GAM337214 and GAM337215

GR147 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 147(GR147) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR147 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The

method by which GR147 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR147 precursor DNA encodes GR147 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR147 is located from position 98930881 to position 98930977 relative to chromosome 12 on the `+` strand.

GR147 precursor RNA folds spatially, forming GR147 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR147 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR147 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR147 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337312 precursor RNA and GAM337313 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337312 RNA and GAM337313 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337312 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337312 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337312 target RNA into GAM337312 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337313 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337313 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337313 target RNA into GAM337313 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR147 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like`

cluster of GR147 polynucleotide: GAM337312 target protein and GAM337313 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337312 and GAM337313

GR148 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 148(GR148) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR148 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR148 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR148 precursor DNA encodes GR148 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR148 is located from position 99096789 to position 99096892 relative to chromosome 12 on the `+` strand.

GR148 precursor RNA folds spatially, forming GR148 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR148 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR148 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR148 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337317 precursor RNA, GAM337318 precursor RNA and GAM337319 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337317 RNA, GAM337318 RNA and GAM337319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337317 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337317 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig. 8, thereby inhibiting translation of GAM337317 target RNA into GAM337317 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337318 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337318 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337318 target RNA into GAM337318 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337319 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337319 target RNA into GAM337319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR148 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR148 polynucleotide: GAM337317 target protein, GAM337318 target protein and GAM337319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337317, GAM337318 and GAM337319

GR149 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 149(GR149) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR149 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR149 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR149 precursor DNA encodes GR149 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR149 is located from position 118768041 to position 118768122 relative to chromosome 12 on the `+` strand.

GR149 precursor RNA folds spatially, forming GR149 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR149 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the

nucleotide sequence of GR149 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR149 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3978 precursor RNA and GAM5048 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3978 RNA and GAM5048 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3978 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3978 target RNA into GAM3978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5048 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5048 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5048 target RNA into GAM5048 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR149 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR149 polynucleotide: GAM3978 target protein and GAM5048 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM3978 and GAM5048

GR150 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 150(GR150) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR150 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR150 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR150 precursor DNA encodes GR150 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR150 is located from position 49044659 to position 49044769 relative to chromosome 12 on the `-` strand.

GR150 precursor RNA folds spatially, forming GR150 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR150 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR150 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR150 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336848 precursor RNA and GAM336849 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336848 RNA and GAM336849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336848 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336848 target RNA into GAM336848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336849 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336849 target RNA into GAM336849 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities,

of GR150 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR150 polynucleotide: GAM336848 target protein and GAM336849 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336848 and GAM336849

GR151 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 151(GR151) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR151 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR151 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR151 precursor DNA encodes GR151 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR151 is located from position 68796420 to position 68796544 relative to chromosome 12 on the `-` strand.

GR151 precursor RNA folds spatially, forming GR151 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR151 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR151 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR151 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM337055 precursor RNA, GAM337056 precursor RNA, GAM337057 precursor RNA and GAM337058 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337055 RNA, GAM337056 RNA, GAM337057 RNA and GAM337058 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337055 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337055 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337055 target RNA into GAM337055 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337056 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337056 target RNA into GAM337056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337057 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337057 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337057 target RNA into GAM337057 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337058 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337058 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337058 target RNA into GAM337058 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR151 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR151 polynucleotide: GAM337055 target protein, GAM337056 target protein, GAM337057 target protein and GAM337058 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337055, GAM337056, GAM337057 and GAM337058

GR152 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 152(GR152) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR152 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR152 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR152 precursor DNA encodes GR152 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR152 is located from position 112469045 to position 112469166 relative to chromosome 12 on the `-` strand.

GR152 precursor RNA folds spatially, forming GR152 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR152 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR152 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR152 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM337430 precursor RNA, GAM337431 precursor RNA, GAM337432 precursor RNA and GAM337433 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337430 RNA, GAM337431 RNA, GAM337432 RNA and GAM337433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337430 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337430 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337430 target RNA into GAM337430 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337431 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337431 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337431 target RNA into GAM337431 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337432 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig. 8, thereby inhibiting translation of GAM337432 target RNA into GAM337432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337433 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337433 target RNA into GAM337433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR152 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR152 polynucleotide: GAM337430 target protein, GAM337431 target protein, GAM337432 target protein and GAM337433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337430, GAM337431, GAM337432 and GAM337433

GR153 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 153(GR153) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR153 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR153 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR153 precursor DNA encodes GR153 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR153 is located from position 116582532 to position 116582633 relative to chromosome 12 on the `-` strand.

GR153 precursor RNA folds spatially, forming GR153 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR153 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR153 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR153 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337456 precursor RNA and GAM337457 precursor RNA,herein

schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337456 RNA and GAM337457 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337456 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337456 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337456 target RNA into GAM337456 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337457 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337457 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337457 target RNA into GAM337457 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR153 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR153 polynucleotide: GAM337456 target protein and GAM337457 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337456 and GAM337457

GR154 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 154(GR154) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR154 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR154 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR154 precursor DNA encodes GR154 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR154 is located from position 132911257

to position 132911356 relative to chromosome 12 on the `-` strand.

GR154 precursor RNA folds spatially, forming GR154 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR154 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR154 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR154 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337555 precursor RNA and GAM337556 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337555 RNA and GAM337556 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337555 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337555 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337555 target RNA into GAM337555 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337556 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337556 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337556 target RNA into GAM337556 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR154 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR154 polynucleotide: GAM337555 target protein and GAM337556 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337555 and GAM337556

GR155 Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory polynucleotide, referred to here as Genomic Record 155(GR155) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR155 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR155 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR155 precursor DNA encodes GR155 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR155 is located from position 96668219 to position 96668344 relative to chromosome 13 on the `-` strand.

GR155 precursor RNA folds spatially, forming GR155 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR155 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR155 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR155 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337285 precursor RNA and GAM337286 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337285 RNA and GAM337286 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337285 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337285 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337285 target RNA into GAM337285 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337286 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337286 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to

a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337286 target RNA into GAM337286 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR155 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR155 polynucleotide: GAM337285 target protein and GAM337286 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337285 and GAM337286

GR156 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 156(GR156) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR156 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR156 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR156 precursor DNA encodes GR156 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR156 is located from position 101658818 to position 101658892 relative to chromosome 13 on the `-` strand.

GR156 precursor RNA folds spatially, forming GR156 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR156 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR156 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR156 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337353 precursor RNA and GAM337354 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337353 RNA and GAM337354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of

Fig. 8.

GAM337353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337353 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337353 target RNA into GAM337353 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337354 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337354 target RNA into GAM337354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR156 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR156 polynucleotide: GAM337353 target protein and GAM337354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337353 and GAM337354

GR157 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 157(GR157) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR157 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR157 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR157 precursor DNA encodes GR157 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR157 is located from position 79670251 to position 79670337 relative to chromosome 14 on the `+` strand.

GR157 precursor RNA folds spatially, forming GR157 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR157 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR157 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a

partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR157 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1820 precursor RNA and GAM3595 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1820 RNA and GAM3595 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1820 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1820 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1820 target RNA into GAM1820 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3595 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3595 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3595 target RNA into GAM3595 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR157 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR157 polynucleotide: GAM1820 target protein and GAM3595 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1820 and GAM3595

GR158 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 158(GR158) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR158 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The

method by which GR158 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR158 precursor DNA encodes GR158 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR158 is located from position 66268768 to position 66268872 relative to chromosome 14 on the `-` strand.

GR158 precursor RNA folds spatially, forming GR158 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR158 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR158 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR158 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337029 precursor RNA and GAM337030 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337029 RNA and GAM337030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337029 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337029 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337029 target RNA into GAM337029 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337030 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337030 target RNA into GAM337030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR158 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like`

cluster of GR158 polynucleotide: GAM337029 target protein and GAM337030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337029 and GAM337030

GR159 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 159(GR159) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR159 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR159 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR159 precursor DNA encodes GR159 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR159 is located from position 101964516 to position 101964622 relative to chromosome 14 on the `-` strand.

GR159 precursor RNA folds spatially, forming GR159 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR159 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR159 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR159 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337358 precursor RNA and GAM337359 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337358 RNA and GAM337359 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337358 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337358 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337358 target RNA into GAM337358

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337359 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337359 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337359 target RNA into GAM337359 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR159 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR159 polynucleotide: GAM337358 target protein and GAM337359 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337358 and GAM337359

GR160 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 160(GR160) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR160 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR160 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR160 precursor DNA encodes GR160 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR160 is located from position 104342178 to position 104342289 relative to chromosome 14 on the `-` strand.

GR160 precursor RNA folds spatially, forming GR160 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR160 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR160 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR160 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337367 precursor RNA and GAM337368 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA

segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337367 RNA and GAM337368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337367 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337367 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337367 target RNA into GAM337367 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337368 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337368 target RNA into GAM337368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR160 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR160 polynucleotide: GAM337367 target protein and GAM337368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337367 and GAM337368

GR161 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 161(GR161) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR161 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR161 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR161 precursor DNA encodes GR161 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR161 is located from position 30068447 to position 30068569 relative to chromosome 15 on the `+` strand.

GR161 precursor RNA folds spatially, forming GR161 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR161 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR161 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR161 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336593 precursor RNA and GAM336594 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336593 RNA and GAM336594 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336593 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336593 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336593 target RNA into GAM336593 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336594 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336594 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336594 target RNA into GAM336594 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR161 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR161 polynucleotide: GAM336593 target protein and GAM336594 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336593 and GAM336594

GR162 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 162(GR162) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like

oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR162 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR162 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR162 precursor DNA encodes GR162 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR162 is located from position 33981295 to position 33981407 relative to chromosome 15 on the `+` strand.

GR162 precursor RNA folds spatially, forming GR162 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR162 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR162 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR162 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3138 precursor RNA and GAM7255 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3138 RNA and GAM7255 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3138 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3138 target RNA into GAM3138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7255 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7255 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7255 target RNA into GAM7255 target

protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR162 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR162 polynucleotide: GAM3138 target protein and GAM7255 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM3138 and GAM7255

GR163 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 163(GR163) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR163 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR163 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR163 precursor DNA encodes GR163 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR163 is located from position 43562097 to position 43562227 relative to chromosome 15 on the `+` strand.

GR163 precursor RNA folds spatially, forming GR163 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR163 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR163 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR163 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM593 precursor RNA and GAM8362 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM593 RNA and GAM8362 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM593 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM593 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM593 target RNA into GAM593 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8362 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8362 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8362 target RNA into GAM8362 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR163 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR163 polynucleotide: GAM593 target protein and GAM8362 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM593 and GAM8362

GR164 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 164(GR164) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR164 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR164 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR164 precursor DNA encodes GR164 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR164 is located from position 56876889 to position 56877003 relative to chromosome 15 on the `+` strand.

GR164 precursor RNA folds spatially, forming GR164 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR164 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR164 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR164 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336917 precursor RNA and GAM336918 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336917 RNA and GAM336918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336917 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336917 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336917 target RNA into GAM336917 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336918 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336918 target RNA into GAM336918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR164 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR164 polynucleotide: GAM336917 target protein and GAM336918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336917 and GAM336918

GR165 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 165(GR165) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR165 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR165 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR165 precursor DNA encodes GR165 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR165 is located from position 97153223 to position 97153320 relative to chromosome 15 on the `+` strand.

GR165 precursor RNA folds spatially, forming GR165 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR165 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR165 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR165 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337293 precursor RNA and GAM337294 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337293 RNA and GAM337294 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337293 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337293 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337293 target RNA into GAM337293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337294 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337294 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337294 target RNA into GAM337294 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR165 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR165 polynucleotide: GAM337293 target protein and GAM337294 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3

TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337293 and GAM337294

GR166 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 166(GR166) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR166 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR166 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR166 precursor DNA encodes GR166 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR166 is located from position 28205837 to position 28205959 relative to chromosome 15 on the `-` strand.

GR166 precursor RNA folds spatially, forming GR166 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR166 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR166 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR166 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM550 precursor RNA and GAM6161 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM550 RNA and GAM6161 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM550 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM550 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM550 target RNA into GAM550 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6161 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6161 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6161 target RNA into GAM6161 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR166 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR166 polynucleotide: GAM550 target protein and GAM6161 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM550 and GAM6161

GR167 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 167(GR167) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR167 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR167 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR167 precursor DNA encodes GR167 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR167 is located from position 12103390 to position 12103474 relative to chromosome 16 on the `+` strand.

GR167 precursor RNA folds spatially, forming GR167 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR167 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR167 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR167 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336380 precursor RNA and GAM336381 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336380 RNA and GAM336381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336380 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336380 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336380 target RNA into GAM336380 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336381 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336381 target RNA into GAM336381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR167 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR167 polynucleotide: GAM336380 target protein and GAM336381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336380 and GAM336381

GR168 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 168(GR168) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR168 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR168 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR168 precursor DNA encodes GR168 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR168 is located from position 30012807 to position 30012916 relative to chromosome 16 on the `+` strand.

GR168 precursor RNA folds spatially, forming GR168 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR168

folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR168 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR168 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1698 precursor RNA and GAM5998 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1698 RNA and GAM5998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1698 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1698 target RNA into GAM1698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5998 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5998 target RNA into GAM5998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR168 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR168 polynucleotide: GAM1698 target protein and GAM5998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1698 and GAM5998

GR169 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 169(GR169) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known

in the art.

GR169 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR169 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR169 precursor DNA encodes GR169 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR169 is located from position 47073422 to position 47073513 relative to chromosome 16 on the `+` strand.

GR169 precursor RNA folds spatially, forming GR169 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR169 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR169 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR169 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336816 precursor RNA and GAM336817 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336816 RNA and GAM336817 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336816 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336816 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336816 target RNA into GAM336816 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336817 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336817 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336817 target RNA into GAM336817 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR169 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR169 polynucleotide: GAM336816 target protein and GAM336817 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336816 and GAM336817

GR170 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 170(GR170) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR170 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR170 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR170 precursor DNA encodes GR170 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR170 is located from position 69762447 to position 69762558 relative to chromosome 16 on the `+` strand.

GR170 precursor RNA folds spatially, forming GR170 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR170 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR170 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR170 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1216 precursor RNA, GAM3479 precursor RNA, GAM7140 precursor RNA and GAM7415 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1216 RNA, GAM3479 RNA, GAM7140 RNA and GAM7415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1216 RNA, herein schematically represented by GAM1 RNA through GAM3

RNA, binds complementarily to a target binding site located in an untranslated region of GAM1216 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1216 target RNA into GAM1216 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3479 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3479 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3479 target RNA into GAM3479 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7140 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7140 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7140 target RNA into GAM7140 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7415 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7415 target RNA into GAM7415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR170 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR170 polynucleotide: GAM1216 target protein, GAM3479 target protein, GAM7140 target protein and GAM7415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1216, GAM3479, GAM7140 and GAM7415

GR171 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 171(GR171) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR171 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The

method by which GR171 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR171 precursor DNA encodes GR171 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR171 is located from position 70140212 to position 70140313 relative to chromosome 16 on the `+` strand.

GR171 precursor RNA folds spatially, forming GR171 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR171 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR171 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR171 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337074 precursor RNA, GAM337075 precursor RNA and GAM337076 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337074 RNA, GAM337075 RNA and GAM337076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337074 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337074 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337074 target RNA into GAM337074 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337075 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337075 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337075 target RNA into GAM337075 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337076 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337076 target RNA into GAM337076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR171 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR171 polynucleotide: GAM337074 target protein, GAM337075 target protein and GAM337076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337074, GAM337075 and GAM337076

GR172 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 172(GR172) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR172 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR172 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR172 precursor DNA encodes GR172 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR172 is located from position 75288695 to position 75288820 relative to chromosome 16 on the `+` strand.

GR172 precursor RNA folds spatially, forming GR172 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR172 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR172 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR172 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4315 precursor RNA and GAM7124 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides

in length, GAM4315 RNA and GAM7124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4315 target RNA into GAM4315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7124 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7124 target RNA into GAM7124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR172 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR172 polynucleotide: GAM4315 target protein and GAM7124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4315 and GAM7124

GR173 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 173(GR173) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR173 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR173 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR173 precursor DNA encodes GR173 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR173 is located from position 77109458 to position 77109568 relative to chromosome 16 on the `+` strand.

GR173 precursor RNA folds spatially, forming GR173 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR173 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the

nucleotide sequence of GR173 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR173 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337180 precursor RNA and GAM337181 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337180 RNA and GAM337181 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337180 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337180 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337180 target RNA into GAM337180 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337181 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337181 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337181 target RNA into GAM337181 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR173 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR173 polynucleotide: GAM337180 target protein and GAM337181 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337180 and GAM337181

GR174 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 174(GR174) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR174 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR174 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR174 precursor DNA encodes GR174 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR174 is located from position 11968201 to position 11968286 relative to chromosome 16 on the `-` strand.

GR174 precursor RNA folds spatially, forming GR174 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR174 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR174 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR174 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336376 precursor RNA and GAM336377 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336376 RNA and GAM336377 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336376 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336376 target RNA into GAM336376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336377 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336377 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336377 target RNA into GAM336377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities,

of GR174 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR174 polynucleotide: GAM336376 target protein and GAM336377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336376 and GAM336377

GR175 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 175(GR175) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR175 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR175 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR175 precursor DNA encodes GR175 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR175 is located from position 48164886 to position 48165017 relative to chromosome 16 on the `-` strand.

GR175 precursor RNA folds spatially, forming GR175 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR175 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR175 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR175 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336833 precursor RNA and GAM336834 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336833 RNA and GAM336834 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336833 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to

a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336833 target RNA into GAM336833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336834 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336834 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336834 target RNA into GAM336834 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR175 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR175 polynucleotide: GAM336833 target protein and GAM336834 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336833 and GAM336834

GR176 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 176(GR176) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR176 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR176 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR176 precursor DNA encodes GR176 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR176 is located from position 1228075 to position 1228162 relative to chromosome 17 on the `+` strand.

GR176 precursor RNA folds spatially, forming GR176 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR176 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR176 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR176 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336255 precursor RNA and GAM336256 precursor RNA,herein

schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336255 RNA and GAM336256 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336255 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336255 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336255 target RNA into GAM336255 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336256 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336256 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336256 target RNA into GAM336256 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR176 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR176 polynucleotide: GAM336255 target protein and GAM336256 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336255 and GAM336256

GR177 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 177(GR177) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR177 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR177 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR177 precursor DNA encodes GR177 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR177 is located from position 4444093

to position 4444184 relative to chromosome 17 on the `+` strand.

GR177 precursor RNA folds spatially, forming GR177 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR177 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR177 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR177 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336282 precursor RNA and GAM336283 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336282 RNA and GAM336283 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336282 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336282 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336282 target RNA into GAM336282 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336283 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336283 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336283 target RNA into GAM336283 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR177 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR177 polynucleotide: GAM336282 target protein and GAM336283 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336282 and GAM336283

GR178 Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory polynucleotide, referred to here as Genomic Record 178(GR178) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR178 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR178 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR178 precursor DNA encodes GR178 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR178 is located from position 8370724 to position 8370825 relative to chromosome 17 on the `+` strand.

GR178 precursor RNA folds spatially, forming GR178 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR178 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR178 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR178 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336320 precursor RNA and GAM336321 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336320 RNA and GAM336321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336320 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336320 target RNA into GAM336320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336321 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to

a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336321 target RNA into GAM336321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR178 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR178 polynucleotide: GAM336320 target protein and GAM336321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336320 and GAM336321

GR179 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 179(GR179) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR179 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR179 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR179 precursor DNA encodes GR179 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR179 is located from position 28064331 to position 28064436 relative to chromosome 17 on the `+` strand.

GR179 precursor RNA folds spatially, forming GR179 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR179 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR179 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR179 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM336567 precursor RNA, GAM336568 precursor RNA and GAM336569 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336567 RNA, GAM336568 RNA and GAM336569 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336567 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336567 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336567 target RNA into GAM336567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336568 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336568 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336568 target RNA into GAM336568 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336569 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336569 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336569 target RNA into GAM336569 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR179 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR179 polynucleotide: GAM336567 target protein, GAM336568 target protein and GAM336569 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336567, GAM336568 and GAM336569

GR180 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 180(GR180) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR180 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR180 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR180 precursor DNA encodes GR180 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR180 is located from position 29086596 to position 29086708 relative to chromosome 17 on the `+` strand.

GR180 precursor RNA folds spatially, forming GR180 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR180 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR180 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR180 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336583 precursor RNA and GAM336584 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336583 RNA and GAM336584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336583 target RNA into GAM336583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336584 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336584 target RNA into GAM336584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR180 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR180 polynucleotide: GAM336583 target protein and GAM336584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336583 and GAM336584

GR181 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 181(GR181) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR181 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR181 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR181 precursor DNA encodes GR181 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR181 is located from position 33138955 to position 33139064 relative to chromosome 17 on the `+` strand.

GR181 precursor RNA folds spatially, forming GR181 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR181 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR181 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR181 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336628 precursor RNA and GAM336629 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336628 RNA and GAM336629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336628 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336628 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336628 target RNA into GAM336628 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM336629 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336629 target RNA into GAM336629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR181 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR181 polynucleotide: GAM336628 target protein and GAM336629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336628 and GAM336629

GR182 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 182(GR182) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR182 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR182 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR182 precursor DNA encodes GR182 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR182 is located from position 38591279 to position 38591402 relative to chromosome 17 on the `+` strand.

GR182 precursor RNA folds spatially, forming GR182 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR182 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR182 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR182 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1653 precursor RNA, GAM1770 precursor RNA and GAM3140 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1653 RNA, GAM1770 RNA and GAM3140 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1653 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1653 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1653 target RNA into GAM1653 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM1770 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1770 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1770 target RNA into GAM1770 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3140 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3140 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3140 target RNA into GAM3140 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR182 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR182 polynucleotide: GAM1653 target protein, GAM1770 target protein and GAM3140 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1653, GAM1770 and GAM3140

GR183 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 183(GR183) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR183 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR183 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR183 precursor DNA encodes GR183 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR183 is located from position 57181803 to position 57181904 relative to chromosome 17 on the `+` strand.

GR183 precursor RNA folds spatially, forming GR183 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR183 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR183 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR183 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336921 precursor RNA and GAM336922 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336921 RNA and GAM336922 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336921 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336921 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336921 target RNA into GAM336921 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336922 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336922 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336922 target RNA into GAM336922 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR183 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR183 polynucleotide: GAM336921 target protein and GAM336922 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with

references to GAM336921 and GAM336922

GR184 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 184(GR184) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR184 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR184 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR184 precursor DNA encodes GR184 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR184 is located from position 58596055 to position 58596161 relative to chromosome 17 on the `+` strand.

GR184 precursor RNA folds spatially, forming GR184 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR184 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR184 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR184 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336937 precursor RNA and GAM336938 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336937 RNA and GAM336938 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336937 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336937 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336937 target RNA into GAM336937 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336938 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336938 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336938 target RNA into GAM336938 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR184 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR184 polynucleotide: GAM336937 target protein and GAM336938 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336937 and GAM336938

GR185 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 185(GR185) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR185 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR185 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR185 precursor DNA encodes GR185 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR185 is located from position 80018909 to position 80019009 relative to chromosome 17 on the `+` strand.

GR185 precursor RNA folds spatially, forming GR185 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR185 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR185 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR185 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337194 precursor RNA and GAM337195 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337194 RNA and GAM337195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337194 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337194 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337194 target RNA into GAM337194 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337195 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337195 target RNA into GAM337195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR185 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR185 polynucleotide: GAM337194 target protein and GAM337195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337194 and GAM337195

GR186 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 186(GR186) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR186 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR186 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR186 precursor DNA encodes GR186 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR186 is located from position 28958697 to position 28958797 relative to chromosome 17 on the `-` strand.

GR186 precursor RNA folds spatially, forming GR186 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR186 folded precursor RNA comprises a plurality of what is known in the art as

`hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR186 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR186 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336578 precursor RNA and GAM336579 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336578 RNA and GAM336579 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336578 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336578 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336578 target RNA into GAM336578 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336579 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336579 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336579 target RNA into GAM336579 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR186 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR186 polynucleotide: GAM336578 target protein and GAM336579 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336578 and GAM336579

GR187 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 187(GR187) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR187 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR187 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR187 precursor DNA encodes GR187 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR187 is located from position 18960647 to position 18960761 relative to chromosome 18 on the `+` strand.

GR187 precursor RNA folds spatially, forming GR187 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR187 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR187 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR187 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336451 precursor RNA and GAM336452 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336451 RNA and GAM336452 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336451 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336451 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336451 target RNA into GAM336451 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336452 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336452 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336452 target RNA into GAM336452 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR187 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR187 polynucleotide: GAM336451 target protein and GAM336452 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336451 and GAM336452

GR188 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 188(GR188) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR188 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR188 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR188 precursor DNA encodes GR188 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR188 is located from position 6790508 to position 6790611 relative to chromosome 19 on the `+` strand.

GR188 precursor RNA folds spatially, forming GR188 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR188 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR188 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR188 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336306 precursor RNA and GAM336307 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336306 RNA and GAM336307 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336306 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336306 target RNA into GAM336306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336307 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336307 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336307 target RNA into GAM336307 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR188 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR188 polynucleotide: GAM336306 target protein and GAM336307 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336306 and GAM336307

GR189 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 189(GR189) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR189 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR189 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR189 precursor DNA encodes GR189 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR189 is located from position 44650568 to position 44650652 relative to chromosome 19 on the `+` strand.

GR189 precursor RNA folds spatially, forming GR189 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR189 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR189 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR189 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate

GAM precursor RNAs, GAM3990 precursor RNA and GAM6994 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3990 RNA and GAM6994 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3990 target RNA into GAM3990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6994 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6994 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6994 target RNA into GAM6994 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR189 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR189 polynucleotide: GAM3990 target protein and GAM6994 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM3990 and GAM6994

GR190 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 190(GR190) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR190 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR190 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR190 precursor DNA encodes GR190 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long. Nucleotide sequence of GR190 is located from position 50818294 to position 50818398 relative to chromosome 19 on the `+` strand.

GR190 precursor RNA folds spatially, forming GR190 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR190 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR190 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR190 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM354 precursor RNA, GAM569 precursor RNA, GAM821 precursor RNA and GAM2911 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM354 RNA, GAM569 RNA, GAM821 RNA and GAM2911 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM354 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM354 target RNA into GAM354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM569 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM569 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM569 target RNA into GAM569 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM821 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM821 target RNA into GAM821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2911 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2911 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2911 target RNA into GAM2911 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR190 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR190 polynucleotide: GAM354 target protein, GAM569 target protein, GAM821 target protein and GAM2911 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM354, GAM569, GAM821 and GAM2911

GR191 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 191(GR191) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR191 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR191 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR191 precursor DNA encodes GR191 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR191 is located from position 54100819 to position 54100905 relative to chromosome 19 on the `+` strand.

GR191 precursor RNA folds spatially, forming GR191 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR191 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR191 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR191 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5512 precursor RNA and GAM5691 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5512 RNA and GAM5691 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5512 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5512 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5512 target RNA into GAM5512 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5691 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5691 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5691 target RNA into GAM5691 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR191 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR191 polynucleotide: GAM5512 target protein and GAM5691 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM5512 and GAM5691

GR192 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 192(GR192) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR192 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR192 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR192 precursor DNA encodes GR192 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR192 is located from position 41616369 to position 41616499 relative to chromosome 19 on the `-` strand.

GR192 precursor RNA folds spatially, forming GR192 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR192 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR192 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR192 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336744 precursor RNA and GAM336745 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336744 RNA and GAM336745 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336744 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336744 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336744 target RNA into GAM336744 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336745 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336745 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336745 target RNA into GAM336745 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR192 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR192 polynucleotide: GAM336744 target protein and GAM336745 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336744 and GAM336745

GR193 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 193(GR193) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR193 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR193 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR193 precursor DNA encodes GR193 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR193 is located from position 108732269 to position 108732372 relative to chromosome 2 on the `+` strand.

GR193 precursor RNA folds spatially, forming GR193 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR193 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR193 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR193 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM337399 precursor RNA, GAM337400 precursor RNA, GAM337401 precursor RNA and GAM337402 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337399 RNA, GAM337400 RNA, GAM337401 RNA and GAM337402 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337399 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337399 target RNA into GAM337399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337400 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337400 target RNA into GAM337400

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337401 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337401 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337401 target RNA into GAM337401 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337402 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337402 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337402 target RNA into GAM337402 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR193 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR193 polynucleotide: GAM337399 target protein, GAM337400 target protein, GAM337401 target protein and GAM337402 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337399, GAM337400, GAM337401 and GAM337402

GR194 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 194(GR194) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR194 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR194 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR194 precursor DNA encodes GR194 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR194 is located from position 131845700 to position 131845801 relative to chromosome 2 on the `+` strand.

GR194 precursor RNA folds spatially, forming GR194 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR194 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR194 precursor RNA comprises a plurality of segments, the

first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR194 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337548 precursor RNA and GAM337549 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337548 RNA and GAM337549 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337548 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337548 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337548 target RNA into GAM337548 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337549 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337549 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337549 target RNA into GAM337549 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR194 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR194 polynucleotide: GAM337548 target protein and GAM337549 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337548 and GAM337549

GR195 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 195(GR195) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR195 precursor DNA, herein designated GR PRECURSOR DNA, is a novel

bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR195 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR195 precursor DNA encodes GR195 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR195 is located from position 20036295 to position 20036386 relative to chromosome 20 on the `+` strand.

GR195 precursor RNA folds spatially, forming GR195 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR195 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR195 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR195 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336469 precursor RNA and GAM336470 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336469 RNA and GAM336470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336469 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336469 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336469 target RNA into GAM336469 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336470 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336470 target RNA into GAM336470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR195 polynucleotide correlate with, and may be deduced from, the identity of

the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR195 polynucleotide: GAM336469 target protein and GAM336470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336469 and GAM336470

GR196 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 196(GR196) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR196 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR196 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR196 precursor DNA encodes GR196 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR196 is located from position 42908008 to position 42908095 relative to chromosome 20 on the `+` strand.

GR196 precursor RNA folds spatially, forming GR196 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR196 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR196 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR196 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336764 precursor RNA and GAM336765 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336764 RNA and GAM336765 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336764 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig. 8, thereby inhibiting translation of GAM336764 target RNA into GAM336764 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336765 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336765 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336765 target RNA into GAM336765 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR196 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR196 polynucleotide: GAM336764 target protein and GAM336765 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336764 and GAM336765

GR197 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 197(GR197) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR197 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR197 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR197 precursor DNA encodes GR197 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR197 is located from position 49549736 to position 49549822 relative to chromosome 20 on the `+` strand.

GR197 precursor RNA folds spatially, forming GR197 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR197 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR197 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR197 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336861 precursor RNA and GAM336862 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED

PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336861 RNA and GAM336862 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336861 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336861 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336861 target RNA into GAM336861 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336862 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336862 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336862 target RNA into GAM336862 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR197 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR197 polynucleotide: GAM336861 target protein and GAM336862 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336861 and GAM336862

GR198 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 198(GR198) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR198 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR198 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR198 precursor DNA encodes GR198 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR198 is located from position 12348835 to position 12348934 relative to chromosome 20 on the `-` strand.

GR198 precursor RNA folds spatially, forming GR198 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR198 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR198 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR198 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336384 precursor RNA and GAM336385 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336384 RNA and GAM336385 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336384 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336384 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336384 target RNA into GAM336384 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336385 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336385 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336385 target RNA into GAM336385 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR198 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR198 polynucleotide: GAM336384 target protein and GAM336385 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336384 and GAM336385

GR199 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 199(GR199)

polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR199 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR199 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR199 precursor DNA encodes GR199 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR199 is located from position 32615342 to position 32615450 relative to chromosome 21 on the `+` strand.

GR199 precursor RNA folds spatially, forming GR199 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR199 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR199 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR199 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM336618 precursor RNA, GAM336619 precursor RNA and GAM336620 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336618 RNA, GAM336619 RNA and GAM336620 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336618 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336618 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336618 target RNA into GAM336618 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336619 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336619 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to

a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336619 target RNA into GAM336619 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336620 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336620 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336620 target RNA into GAM336620 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR199 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR199 polynucleotide: GAM336618 target protein, GAM336619 target protein and GAM336620 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336618, GAM336619 and GAM336620

GR200 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 200(GR200) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR200 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR200 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR200 precursor DNA encodes GR200 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR200 is located from position 44376402 to position 44376497 relative to chromosome 21 on the `+` strand.

GR200 precursor RNA folds spatially, forming GR200 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR200 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR200 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR200 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate

GAM precursor RNAs, GAM336781 precursor RNA and GAM336782 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336781 RNA and GAM336782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336781 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336781 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336781 target RNA into GAM336781 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336782 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336782 target RNA into GAM336782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR200 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR200 polynucleotide: GAM336781 target protein and GAM336782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336781 and GAM336782

GR201 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 201(GR201) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR201 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR201 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR201 precursor DNA encodes GR201 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long. Nucleotide sequence of GR201 is located from position 24199772 to position 24199866 relative to chromosome 22 on the `+` strand.

GR201 precursor RNA folds spatially, forming GR201 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR201 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR201 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR201 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336528 precursor RNA and GAM336529 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336528 RNA and GAM336529 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336528 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336528 target RNA into GAM336528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336529 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336529 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336529 target RNA into GAM336529 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR201 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR201 polynucleotide: GAM336528 target protein and GAM336529 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336528 and GAM336529

GR202 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 202(GR202) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR202 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR202 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR202 precursor DNA encodes GR202 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR202 is located from position 9793682 to position 9793766 relative to chromosome 3 on the `+` strand.

GR202 precursor RNA folds spatially, forming GR202 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR202 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR202 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR202 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM336341 precursor RNA, GAM336342 precursor RNA and GAM336343 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336341 RNA, GAM336342 RNA and GAM336343 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336341 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336341 target RNA into GAM336341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336342 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM336342 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336342 target RNA into GAM336342 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336343 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336343 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336343 target RNA into GAM336343 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR202 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR202 polynucleotide: GAM336341 target protein, GAM336342 target protein and GAM336343 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336341, GAM336342 and GAM336343

GR203 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 203(GR203) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR203 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR203 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR203 precursor DNA encodes GR203 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR203 is located from position 40002861 to position 40002950 relative to chromosome 4 on the `+` strand.

GR203 precursor RNA folds spatially, forming GR203 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR203 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR203 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR203 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336716 precursor RNA and GAM336717 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336716 RNA and GAM336717 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336716 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336716 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336716 target RNA into GAM336716 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336717 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336717 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336717 target RNA into GAM336717 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR203 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR203 polynucleotide: GAM336716 target protein and GAM336717 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336716 and GAM336717

GR204 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 204(GR204) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR204 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR204 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR204 precursor DNA encodes GR204 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR204 is located from position 95449990 to position 95450088 relative to chromosome 4 on the `+` strand.

GR204 precursor RNA folds spatially, forming GR204 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR204 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR204 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR204 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM189 precursor RNA and GAM3190 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM189 RNA and GAM3190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189 target RNA into GAM189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3190 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3190 target RNA into GAM3190 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR204 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR204 polynucleotide: GAM189 target protein and GAM3190 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with

references to GAM189 and GAM3190

GR205 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 205(GR205) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR205 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR205 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR205 precursor DNA encodes GR205 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR205 is located from position 7755711 to position 7755813 relative to chromosome 5 on the `+` strand.

GR205 precursor RNA folds spatially, forming GR205 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR205 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR205 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR205 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM336315 precursor RNA, GAM336316 precursor RNA and GAM336317 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336315 RNA, GAM336316 RNA and GAM336317 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336315 target RNA into GAM336315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336316 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336316 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336316 target RNA into GAM336316 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336317 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336317 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336317 target RNA into GAM336317 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR205 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR205 polynucleotide: GAM336315 target protein, GAM336316 target protein and GAM336317 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336315, GAM336316 and GAM336317

GR206 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 206(GR206) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR206 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR206 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR206 precursor DNA encodes GR206 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR206 is located from position 69818313 to position 69818412 relative to chromosome 5 on the `+` strand.

GR206 precursor RNA folds spatially, forming GR206 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR206 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR206 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is

well known in the art.

GR206 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337069 precursor RNA and GAM337070 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337069 RNA and GAM337070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337069 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337069 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337069 target RNA into GAM337069 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337070 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337070 target RNA into GAM337070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR206 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR206 polynucleotide: GAM337069 target protein and GAM337070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337069 and GAM337070

GR207 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 207(GR207) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR207 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR207 precursor DNA was detected is described hereinabove with

additional reference to Figs. 8-18.

GR207 precursor DNA encodes GR207 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR207 is located from position 70361144 to position 70361243 relative to chromosome 5 on the `+` strand.

GR207 precursor RNA folds spatially, forming GR207 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR207 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR207 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR207 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337081 precursor RNA and GAM337082 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337081 RNA and GAM337082 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337081 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337081 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337081 target RNA into GAM337081 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337082 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337082 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337082 target RNA into GAM337082 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR207 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR207 polynucleotide: GAM337081 target protein and GAM337082 target

protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337081 and GAM337082

GR208 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 208(GR208) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR208 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR208 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR208 precursor DNA encodes GR208 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR208 is located from position 69076604 to position 69076703 relative to chromosome 5 on the `-` strand.

GR208 precursor RNA folds spatially, forming GR208 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR208 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR208 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR208 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM689 precursor RNA and GAM337060 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM689 RNA and GAM337060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM689 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM689 target RNA into GAM689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3

TARGET PROTEIN, both of Fig. 8.

GAM337060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337060 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337060 target RNA into GAM337060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR208 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR208 polynucleotide: GAM689 target protein and GAM337060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM689 and GAM337060

GR209 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 209(GR209) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR209 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR209 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR209 precursor DNA encodes GR209 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR209 is located from position 30850314 to position 30850405 relative to chromosome 6 on the `+` strand.

GR209 precursor RNA folds spatially, forming GR209 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR209 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR209 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR209 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5990 precursor RNA and GAM6459 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5990 RNA and GAM6459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5990 target RNA into GAM5990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6459 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6459 target RNA into GAM6459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR209 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR209 polynucleotide: GAM5990 target protein and GAM6459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM5990 and GAM6459

GR210 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 210(GR210) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR210 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR210 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR210 precursor DNA encodes GR210 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR210 is located from position 31554609 to position 31554710 relative to chromosome 6 on the `+` strand.

GR210 precursor RNA folds spatially, forming GR210 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR210 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR210 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR210 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336607 precursor RNA and GAM336608 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336607 RNA and GAM336608 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336607 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336607 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336607 target RNA into GAM336607 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336608 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336608 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336608 target RNA into GAM336608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR210 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR210 polynucleotide: GAM336607 target protein and GAM336608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336607 and GAM336608

GR211 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 211(GR211) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR211 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR211 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR211 precursor DNA encodes GR211 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR211 is located from position 17062054 to position 17062168 relative to chromosome 7 on the `+` strand.

GR211 precursor RNA folds spatially, forming GR211 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR211 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR211 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR211 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336430 precursor RNA and GAM336431 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336430 RNA and GAM336431 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336430 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336430 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336430 target RNA into GAM336430 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336431 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336431 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336431 target RNA into GAM336431 target protein, herein schematically represented by GAM1 TARGET PROTEIN through

GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR211 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR211 polynucleotide: GAM336430 target protein and GAM336431 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336430 and GAM336431

GR212 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 212(GR212) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR212 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR212 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR212 precursor DNA encodes GR212 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR212 is located from position 29435833 to position 29435938 relative to chromosome 7 on the `+` strand.

GR212 precursor RNA folds spatially, forming GR212 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR212 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR212 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR212 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336587 precursor RNA and GAM336588 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336587 RNA and GAM336588 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336587 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336587 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336587 target RNA into GAM336587 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336588 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336588 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336588 target RNA into GAM336588 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR212 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR212 polynucleotide: GAM336587 target protein and GAM336588 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336587 and GAM336588

GR213 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 213(GR213) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR213 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR213 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR213 precursor DNA encodes GR213 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR213 is located from position 65815377 to position 65815469 relative to chromosome 7 on the `+` strand.

GR213 precursor RNA folds spatially, forming GR213 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR213 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR213 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR213 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337023 precursor RNA and GAM337024 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337023 RNA and GAM337024 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337023 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337023 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337023 target RNA into GAM337023 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337024 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337024 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337024 target RNA into GAM337024 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR213 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR213 polynucleotide: GAM337023 target protein and GAM337024 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337023 and GAM337024

GR214 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 214(GR214) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR214 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR214 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR214 precursor DNA encodes GR214 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR214 is located from position 72274763 to position 72274861 relative to chromosome 7 on the `+` strand.

GR214 precursor RNA folds spatially, forming GR214 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR214 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR214 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR214 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337111 precursor RNA, GAM337112 precursor RNA and GAM337113 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337111 RNA, GAM337112 RNA and GAM337113 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337111 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337111 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337111 target RNA into GAM337111 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337112 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337112 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337112 target RNA into GAM337112 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337113 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337113 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337113 target RNA into GAM337113

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR214 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR214 polynucleotide: GAM337111 target protein, GAM337112 target protein and GAM337113 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337111, GAM337112 and GAM337113

GR215 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 215(GR215) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR215 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR215 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR215 precursor DNA encodes GR215 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR215 is located from position 73215042 to position 73215142 relative to chromosome 7 on the `+` strand.

GR215 precursor RNA folds spatially, forming GR215 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR215 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR215 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR215 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337127 precursor RNA and GAM337128 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337127 RNA and GAM337128 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337127 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337127 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337127 target RNA into GAM337127 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337128 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337128 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337128 target RNA into GAM337128 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR215 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR215 polynucleotide: GAM337127 target protein and GAM337128 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337127 and GAM337128

GR216 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 216(GR216) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR216 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR216 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR216 precursor DNA encodes GR216 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR216 is located from position 78652714 to position 78652815 relative to chromosome 7 on the `+` strand.

GR216 precursor RNA folds spatially, forming GR216 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR216 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR216 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is

well known in the art.

GR216 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337188 precursor RNA and GAM337189 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337188 RNA and GAM337189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337188 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337188 target RNA into GAM337188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337189 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337189 target RNA into GAM337189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR216 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR216 polynucleotide: GAM337188 target protein and GAM337189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337188 and GAM337189

GR217 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 217(GR217) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR217 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR217 precursor DNA was detected is described hereinabove with

additional reference to Figs. 8-18.

GR217 precursor DNA encodes GR217 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR217 is located from position 84223987 to position 84224087 relative to chromosome 7 on the `+` strand.

GR217 precursor RNA folds spatially, forming GR217 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR217 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR217 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR217 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337207 precursor RNA and GAM337208 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337207 RNA and GAM337208 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337207 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337207 target RNA into GAM337207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337208 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337208 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337208 target RNA into GAM337208 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR217 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR217 polynucleotide: GAM337207 target protein and GAM337208 target

protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337207 and GAM337208

GR218 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 218(GR218) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR218 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR218 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR218 precursor DNA encodes GR218 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR218 is located from position 98227794 to position 98227886 relative to chromosome 7 on the `+` strand.

GR218 precursor RNA folds spatially, forming GR218 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR218 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR218 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR218 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337299 precursor RNA and GAM337300 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337299 RNA and GAM337300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337299 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337299 target RNA into GAM337299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through

GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337300 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337300 target RNA into GAM337300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR218 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR218 polynucleotide: GAM337299 target protein and GAM337300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337299 and GAM337300

GR219 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 219(GR219) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR219 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR219 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR219 precursor DNA encodes GR219 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR219 is located from position 104082522 to position 104082645 relative to chromosome 7 on the `+` strand.

GR219 precursor RNA folds spatially, forming GR219 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR219 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR219 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR219 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6440 precursor RNA and GAM7095 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6440 RNA and GAM7095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6440 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6440 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6440 target RNA into GAM6440 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7095 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7095 target RNA into GAM7095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR219 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR219 polynucleotide: GAM6440 target protein and GAM7095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM6440 and GAM7095

GR220 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 220(GR220) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR220 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR220 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR220 precursor DNA encodes GR220 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR220 is located from position 113861407 to position 113861497 relative to chromosome 7 on the `+` strand.

GR220 precursor RNA folds spatially, forming GR220 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR220 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR220 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR220 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337446 precursor RNA, GAM337447 precursor RNA and GAM337448 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337446 RNA, GAM337447 RNA and GAM337448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337446 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337446 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337446 target RNA into GAM337446 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337447 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337447 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337447 target RNA into GAM337447 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337448 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337448 target RNA into GAM337448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR220 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like`

cluster of GR220 polynucleotide: GAM337446 target protein, GAM337447 target protein and GAM337448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337446, GAM337447 and GAM337448

GR221 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 221(GR221) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR221 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR221 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR221 precursor DNA encodes GR221 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR221 is located from position 133099401 to position 133099515 relative to chromosome 7 on the `+` strand.

GR221 precursor RNA folds spatially, forming GR221 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR221 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR221 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR221 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1942 precursor RNA, GAM5329 precursor RNA and GAM6271 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1942 RNA, GAM5329 RNA and GAM6271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1942 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1942 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1942 target RNA into GAM1942 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5329 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5329 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5329 target RNA into GAM5329 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6271 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6271 target RNA into GAM6271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR221 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR221 polynucleotide: GAM1942 target protein, GAM5329 target protein and GAM6271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1942, GAM5329 and GAM6271

GR222 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 222(GR222) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR222 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR222 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR222 precursor DNA encodes GR222 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR222 is located from position 66122717 to position 66122818 relative to chromosome 7 on the `-` strand.

GR222 precursor RNA folds spatially, forming GR222 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR222 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the

nucleotide sequence of GR222 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR222 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337027 precursor RNA and GAM337028 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337027 RNA and GAM337028 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337027 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337027 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337027 target RNA into GAM337027 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337028 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337028 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337028 target RNA into GAM337028 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR222 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR222 polynucleotide: GAM337027 target protein and GAM337028 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337027 and GAM337028

GR223 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 223(GR223) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR223 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR223 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR223 precursor DNA encodes GR223 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR223 is located from position 12908963 to position 12909066 relative to chromosome 8 on the `+` strand.

GR223 precursor RNA folds spatially, forming GR223 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR223 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR223 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR223 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336394 precursor RNA and GAM336395 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336394 RNA and GAM336395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336394 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336394 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336394 target RNA into GAM336394 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336395 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336395 target RNA into GAM336395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities,

of GR223 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR223 polynucleotide: GAM336394 target protein and GAM336395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336394 and GAM336395

GR224 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 224(GR224) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR224 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR224 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR224 precursor DNA encodes GR224 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR224 is located from position 21935927 to position 21936034 relative to chromosome 8 on the `+` strand.

GR224 precursor RNA folds spatially, forming GR224 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR224 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR224 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR224 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336497 precursor RNA and GAM336498 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336497 RNA and GAM336498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336497 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336497 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to

a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336497 target RNA into GAM336497 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336498 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336498 target RNA into GAM336498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR224 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR224 polynucleotide: GAM336497 target protein and GAM336498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336497 and GAM336498

GR225 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 225(GR225) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR225 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR225 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR225 precursor DNA encodes GR225 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR225 is located from position 41616885 to position 41616976 relative to chromosome 8 on the `+` strand.

GR225 precursor RNA folds spatially, forming GR225 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR225 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR225 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR225 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336746 precursor RNA and GAM336747 precursor RNA,herein

schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336746 RNA and GAM336747 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336746 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336746 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336746 target RNA into GAM336746 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336747 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336747 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336747 target RNA into GAM336747 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR225 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR225 polynucleotide: GAM336746 target protein and GAM336747 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336746 and GAM336747

GR226 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 226(GR226) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR226 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR226 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR226 precursor DNA encodes GR226 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR226 is located from position 54026269

to position 54026340 relative to chromosome 8 on the `+` strand.

GR226 precursor RNA folds spatially, forming GR226 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR226 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR226 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR226 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2171 precursor RNA and GAM6531 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2171 RNA and GAM6531 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2171 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2171 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2171 target RNA into GAM2171 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6531 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6531 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6531 target RNA into GAM6531 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR226 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR226 polynucleotide: GAM2171 target protein and GAM6531 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM2171 and GAM6531

GR227 Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory polynucleotide, referred to here as Genomic Record 227(GR227) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR227 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR227 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR227 precursor DNA encodes GR227 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR227 is located from position 101882283 to position 101882352 relative to chromosome 8 on the `+` strand.

GR227 precursor RNA folds spatially, forming GR227 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR227 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR227 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR227 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5082 precursor RNA and GAM7700 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5082 RNA and GAM7700 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5082 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5082 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5082 target RNA into GAM5082 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7700 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7700 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7700 target RNA into GAM7700 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR227 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR227 polynucleotide: GAM5082 target protein and GAM7700 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM5082 and GAM7700

GR228 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 228(GR228) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR228 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR228 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR228 precursor DNA encodes GR228 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR228 is located from position 141572888 to position 141572989 relative to chromosome 8 on the `+` strand.

GR228 precursor RNA folds spatially, forming GR228 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR228 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR228 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR228 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337586 precursor RNA and GAM337587 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337586 RNA and GAM337587 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of

Fig. 8.

GAM337586 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337586 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337586 target RNA into GAM337586 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337587 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337587 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337587 target RNA into GAM337587 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR228 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR228 polynucleotide: GAM337586 target protein and GAM337587 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337586 and GAM337587

GR229 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 229(GR229) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR229 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR229 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR229 precursor DNA encodes GR229 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR229 is located from position 10822733 to position 10822834 relative to chromosome 8 on the `-` strand.

GR229 precursor RNA folds spatially, forming GR229 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR229 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR229 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a

partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR229 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336359 precursor RNA and GAM336360 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336359 RNA and GAM336360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336359 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336359 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336359 target RNA into GAM336359 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336360 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336360 target RNA into GAM336360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR229 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR229 polynucleotide: GAM336359 target protein and GAM336360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336359 and GAM336360

GR230 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 230(GR230) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR230 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The

method by which GR230 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR230 precursor DNA encodes GR230 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR230 is located from position 53863297 to position 53863389 relative to chromosome 8 on the `-` strand.

GR230 precursor RNA folds spatially, forming GR230 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR230 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR230 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR230 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336894 precursor RNA and GAM336895 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336894 RNA and GAM336895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336894 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336894 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336894 target RNA into GAM336894 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336895 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336895 target RNA into GAM336895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR230 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like`

cluster of GR230 polynucleotide: GAM336894 target protein and GAM336895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336894 and GAM336895

GR231 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 231(GR231) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR231 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR231 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR231 precursor DNA encodes GR231 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR231 is located from position 106717983 to position 106718084 relative to chromosome 8 on the `-` strand.

GR231 precursor RNA folds spatially, forming GR231 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR231 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR231 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR231 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337388 precursor RNA and GAM337389 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337388 RNA and GAM337389 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337388 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337388 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337388 target RNA into GAM337388

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337389 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337389 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337389 target RNA into GAM337389 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR231 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR231 polynucleotide: GAM337388 target protein and GAM337389 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337388 and GAM337389

GR232 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 232(GR232) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR232 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR232 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR232 precursor DNA encodes GR232 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR232 is located from position 132744616 to position 132744727 relative to chromosome 8 on the `-` strand.

GR232 precursor RNA folds spatially, forming GR232 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR232 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR232 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR232 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337553 precursor RNA and GAM337554 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA

segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337553 RNA and GAM337554 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337553 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337553 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337553 target RNA into GAM337553 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337554 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337554 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337554 target RNA into GAM337554 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR232 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR232 polynucleotide: GAM337553 target protein and GAM337554 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337553 and GAM337554

GR233 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 233(GR233) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR233 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR233 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR233 precursor DNA encodes GR233 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR233 is located from position 135501500 to position 135501600 relative to chromosome 8 on the `-` strand.

GR233 precursor RNA folds spatially, forming GR233 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR233 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR233 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR233 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337567 precursor RNA, GAM337568 precursor RNA and GAM337569 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337567 RNA, GAM337568 RNA and GAM337569 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337567 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337567 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337567 target RNA into GAM337567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337568 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337568 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337568 target RNA into GAM337568 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337569 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337569 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337569 target RNA into GAM337569 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR233 polynucleotide correlate with, and may be deduced from, the identity of

the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR233 polynucleotide: GAM337567 target protein, GAM337568 target protein and GAM337569 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337567, GAM337568 and GAM337569

GR234 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 234(GR234) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR234 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR234 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR234 precursor DNA encodes GR234 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR234 is located from position 141088822 to position 141088915 relative to chromosome 8 on the `-` strand.

GR234 precursor RNA folds spatially, forming GR234 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR234 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR234 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR234 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337584 precursor RNA and GAM337585 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337584 RNA and GAM337585 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337584 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to

a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337584 target RNA into GAM337584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337585 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337585 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337585 target RNA into GAM337585 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR234 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR234 polynucleotide: GAM337584 target protein and GAM337585 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337584 and GAM337585

GR235 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 235(GR235) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR235 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR235 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR235 precursor DNA encodes GR235 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR235 is located from position 6225060 to position 6225156 relative to chromosome 9 on the `+` strand.

GR235 precursor RNA folds spatially, forming GR235 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR235 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR235 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR235 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336299 precursor RNA and GAM336300 precursor RNA,herein

schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336299 RNA and GAM336300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336299 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336299 target RNA into GAM336299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336300 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336300 target RNA into GAM336300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR235 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR235 polynucleotide: GAM336299 target protein and GAM336300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336299 and GAM336300

GR236 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 236(GR236) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR236 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR236 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR236 precursor DNA encodes GR236 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR236 is located from position 37420113

to position 37422669 relative to chromosome 9 on the `+` strand.

GR236 precursor RNA folds spatially, forming GR236 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR236 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR236 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR236 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM329 precursor RNA and GAM336681 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM329 RNA and GAM336681 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM329 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM329 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM329 target RNA into GAM329 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336681 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336681 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336681 target RNA into GAM336681 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR236 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR236 polynucleotide: GAM329 target protein and GAM336681 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM329 and GAM336681

GR237 Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory polynucleotide, referred to here as Genomic Record 237(GR237) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR237 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR237 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR237 precursor DNA encodes GR237 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR237 is located from position 66974964 to position 66975069 relative to chromosome 9 on the `+` strand.

GR237 precursor RNA folds spatially, forming GR237 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR237 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR237 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR237 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337037 precursor RNA, GAM337038 precursor RNA and GAM337039 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337037 RNA, GAM337038 RNA and GAM337039 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337037 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337037 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337037 target RNA into GAM337037 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337038 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337038 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337038 target RNA into GAM337038 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337039 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337039 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337039 target RNA into GAM337039 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR237 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR237 polynucleotide: GAM337037 target protein, GAM337038 target protein and GAM337039 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337037, GAM337038 and GAM337039

GR238 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 238(GR238) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR238 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR238 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR238 precursor DNA encodes GR238 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR238 is located from position 78004551 to position 78004659 relative to chromosome 9 on the `+` strand.

GR238 precursor RNA folds spatially, forming GR238 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR238 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR238 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR238 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA,

is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2306 precursor RNA and GAM6265 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2306 RNA and GAM6265 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2306 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2306 target RNA into GAM2306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6265 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6265 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6265 target RNA into GAM6265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR238 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR238 polynucleotide: GAM2306 target protein and GAM6265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM2306 and GAM6265

GR239 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 239(GR239) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR239 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR239 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR239 precursor DNA encodes GR239 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR239 is located from position 88520248 to position 88520363 relative to chromosome 9 on the `+` strand.

GR239 precursor RNA folds spatially, forming GR239 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR239 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR239 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR239 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1217 precursor RNA, GAM3461 precursor RNA, GAM4557 precursor RNA and GAM7636 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1217 RNA, GAM3461 RNA, GAM4557 RNA and GAM7636 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1217 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1217 target RNA into GAM1217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3461 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3461 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3461 target RNA into GAM3461 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4557 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4557 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4557 target RNA into GAM4557 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3

TARGET PROTEIN, both of Fig. 8.

GAM7636 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7636 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7636 target RNA into GAM7636 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR239 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR239 polynucleotide: GAM1217 target protein, GAM3461 target protein, GAM4557 target protein and GAM7636 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM1217, GAM3461, GAM4557 and GAM7636

GR240 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 240(GR240) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR240 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR240 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR240 precursor DNA encodes GR240 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR240 is located from position 93648456 to position 93648553 relative to chromosome 9 on the `+` strand.

GR240 precursor RNA folds spatially, forming GR240 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR240 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR240 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR240 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337264 precursor RNA, GAM337265 precursor RNA and GAM337266 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs

being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337264 RNA, GAM337265 RNA and GAM337266 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337264 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337264 target RNA into GAM337264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337265 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337265 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337265 target RNA into GAM337265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337266 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337266 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337266 target RNA into GAM337266 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR240 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR240 polynucleotide: GAM337264 target protein, GAM337265 target protein and GAM337266 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337264, GAM337265 and GAM337266

GR241 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 241(GR241) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR241 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR241 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR241 precursor DNA encodes GR241 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR241 is located from position 106800362 to position 106800470 relative to chromosome 9 on the `+` strand.

GR241 precursor RNA folds spatially, forming GR241 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR241 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR241 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR241 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337390 precursor RNA and GAM337391 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337390 RNA and GAM337391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337390 target RNA into GAM337390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337391 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337391 target RNA into GAM337391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities,

of GR241 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR241 polynucleotide: GAM337390 target protein and GAM337391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337390 and GAM337391

GR242 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 242(GR242) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR242 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR242 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR242 precursor DNA encodes GR242 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR242 is located from position 117327121 to position 117327213 relative to chromosome 9 on the `+` strand.

GR242 precursor RNA folds spatially, forming GR242 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR242 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR242 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR242 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337463 precursor RNA and GAM337464 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337463 RNA and GAM337464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337463 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337463 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to

a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337463 target RNA into GAM337463 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337464 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337464 target RNA into GAM337464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR242 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR242 polynucleotide: GAM337463 target protein and GAM337464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337463 and GAM337464

GR243 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 243(GR243) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR243 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR243 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR243 precursor DNA encodes GR243 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR243 is located from position 47243042 to position 47243138 relative to chromosome X on the `+` strand.

GR243 precursor RNA folds spatially, forming GR243 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR243 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR243 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR243 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3768 precursor RNA and GAM5422 precursor RNA,herein

schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3768 RNA and GAM5422 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3768 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3768 target RNA into GAM3768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5422 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5422 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5422 target RNA into GAM5422 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR243 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR243 polynucleotide: GAM3768 target protein and GAM5422 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM3768 and GAM5422

GR244 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 244(GR244) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR244 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR244 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR244 precursor DNA encodes GR244 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR244 is located from position 77528890

to position 77528959 relative to chromosome X on the `+` strand.

GR244 precursor RNA folds spatially, forming GR244 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR244 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR244 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR244 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4130 precursor RNA and GAM8439 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4130 RNA and GAM8439 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4130 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4130 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4130 target RNA into GAM4130 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8439 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8439 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8439 target RNA into GAM8439 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR244 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR244 polynucleotide: GAM4130 target protein and GAM8439 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM4130 and GAM8439

GR245 Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory polynucleotide, referred to here as Genomic Record 245(GR245) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR245 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR245 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR245 precursor DNA encodes GR245 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR245 is located from position 94524959 to position 94525061 relative to chromosome X on the `+` strand.

GR245 precursor RNA folds spatially, forming GR245 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR245 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR245 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR245 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM361 precursor RNA and GAM4707 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM361 RNA and GAM4707 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM361 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM361 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM361 target RNA into GAM361 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4707 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4707 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4707 target RNA into GAM4707 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR245 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR245 polynucleotide: GAM361 target protein and GAM4707 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM361 and GAM4707

GR246 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 246(GR246) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR246 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR246 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR246 precursor DNA encodes GR246 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR246 is located from position 98459191 to position 98459278 relative to chromosome X on the `+` strand.

GR246 precursor RNA folds spatially, forming GR246 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR246 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR246 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR246 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337303 precursor RNA and GAM337304 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337303 RNA and GAM337304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of

Fig. 8.

GAM337303 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337303 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337303 target RNA into GAM337303 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337304 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337304 target RNA into GAM337304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR246 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR246 polynucleotide: GAM337303 target protein and GAM337304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337303 and GAM337304

GR247 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 247(GR247) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR247 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR247 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR247 precursor DNA encodes GR247 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR247 is located from position 107483900 to position 107487923 relative to chromosome X on the `+` strand.

GR247 precursor RNA folds spatially, forming GR247 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR247 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR247 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a

partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR247 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5254 precursor RNA and GAM8339 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5254 RNA and GAM8339 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5254 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5254 target RNA into GAM5254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8339 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8339 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8339 target RNA into GAM8339 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR247 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR247 polynucleotide: GAM5254 target protein and GAM8339 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM5254 and GAM8339

GR248 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 248(GR248) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR248 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The

method by which GR248 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR248 precursor DNA encodes GR248 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR248 is located from position 148876208 to position 148876293 relative to chromosome X on the `+` strand.

GR248 precursor RNA folds spatially, forming GR248 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR248 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR248 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR248 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM337601 precursor RNA and GAM337602 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337601 RNA and GAM337602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337601 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337601 target RNA into GAM337601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM337602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337602 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337602 target RNA into GAM337602 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR248 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like`

cluster of GR248 polynucleotide: GAM337601 target protein and GAM337602 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM337601 and GAM337602

GR249 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory polynucleotide, referred to here as Genomic Record 249(GR249) polynucleotide, which encodes an `operon-like` cluster of novel micro RNA-like oligonucleotides, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR249 precursor DNA, herein designated GR PRECURSOR DNA, is a novel bioinformatically detected regulatory, non protein coding polynucleotide. The method by which GR249 precursor DNA was detected is described hereinabove with additional reference to Figs. 8-18.

GR249 precursor DNA encodes GR249 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long. Nucleotide sequence of GR249 is located from position 44431916 to position 44432023 relative to chromosome X on the `-` strand.

GR249 precursor RNA folds spatially, forming GR249 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR249 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR249 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial or accurate reverse-complement sequence of the second half thereof, as is well known in the art.

GR249 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336783 precursor RNA and GAM336784 precursor RNA,herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336783 RNA and GAM336784 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM336783 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336783 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336783 target RNA into GAM336783

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336784 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336784 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336784 target RNA into GAM336784 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR249 polynucleotide correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR249 polynucleotide: GAM336783 target protein and GAM336784 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated in Table 8, with references to GAM336783 and GAM336784

| ROW# | DISEASE NAME | TARGET-GENES ASSOCIATED WITH ALZHEIMER DISEASE |
|---|---|---|
| 1 | ALL | PLAU, CNTF, AVP, CRYAB, SNCB, APBA2, DHCR24, CTNND2, PSEN1, APLP1, GSK3B, APPBP2, DSCR1, MME, CRAT, AGER, NCSTN, ABCD1, BCHE, A2M, MTNR1A, APOC1, THOP1, APBA1, SERPINA3, ACHE, UBB, PIN1, TNFSF5, ADAM17, BACE2, PLCD1, APLP2, CTSK, BACE, SOD2, ADAM10, DLST, CTSG, NPY, OGDH, GYPA, PRND, CHAT, PSEN2, ACE, RAGE, GAL, APBB1, TRPM2, GSN, SNCA, BLMH, IL1A, TNFRSF6, HADH2, FHL2, ARHA, MAPK10, SLC6A4, OLR1, TGFB1, FLNB, TNF, ADAMTS5, SNCAIP, SNCG, MAPT, TFCP2, TNFRSF5, IAPP, CLU, B2M, VLDLR, GLUL, CAV2, IDE, NCKAP1, APBB2, FOS, ESR2, ACT, NGB, FPRL1, HTR2C, APCS, IGF1, CASP3, IL1B, HTR2A, GFAP, CRH, APP, SLC17A7, LRP1, PRNP, MPO, NOTCH1, S100B, MT3, CAV1, HD, BAX and CTSB. |
| 2 | Alzheimer | AVP, NCSTN, ARHA, APPBP2, HTR2A, PSEN1, DHCR24, PLAU, MTNR1A, SERPINA3, DSCR1, APBA1, APOC1, BCHE, MME, BACE2, UBB, CTNND2, APLP1, APP, SLC17A7, NCKAP1, GFAP, IGF1, SLC6A4, HD, S100B, CASP3, MPO, CNTF, GSK3B, CRH, LRP1, MT3, APBA2, CAV1, CRYAB, MAPK10, TGFB1, CHAT, TNFRSF5, CTSB, MAPT, OLR1, FLNB, CAV2, GLUL, IAPP, NGB, ACT, FOS, APBB2, TNF, SNCAIP, APLP2, PSEN2, OGDH, GYPA, ADAM17, ADAM10, ADAMTS5, BACE, TNFRSF6, ACE, HTR2C, RAGE, HADH2, FHL2, PRND, IL1A, SNCA, DLST, CTSK, TRPM2, BLMH. |